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OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 09:53:38 ; Search time 86 Seconds  
(without alignments)  
209.291 Million cell updates/sec

Title: US-10-070-588A-112  
Perfect score: 11  
Sequence: 1 ctttggcacta 11

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents\_NA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	11	100.0	207	4	US-09-248-796A-8315, A
6	11	100.0	276	4	US-09-513-999C-27111, A
7	11	100.0	305	4	US-09-270-767-26937, A
8	11	100.0	321	4	US-09-543-681A-963, A
9	11	100.0	341	4	US-09-513-999C-3625, A
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12	11	100.0	396	4	US-09-640-173-30, A
13	11	100.0	396	4	US-09-713-550-30, A
14	11	100.0	396	4	US-09-825-294-30, A
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18	11	100.0	477	4	US-09-248-796A-2902, A
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c 252	11	100.0	4699	3	US-08-474-671-1	Sequence 1, Appli	325	11	100.0	9370	5	PCT-US94-04496-27	Sequence 27, Appli
c 253	11	100.0	4699	3	US-08-483-577A-1	Sequence 1, Appli	326	11	100.0	9391	1	US-08-320-559-25	Sequence 25, Appli
c 254	11	100.0	4699	3	US-08-897-438-1	Sequence 1, Appli	327	11	100.0	9391	3	US-08-545-860D-25	Sequence 25, Appli
c 255	11	100.0	4699	3	US-08-637-654-1	Sequence 1, Appli	328	11	100.0	9391	5	PCT-US94-04496-25	Sequence 25, Appli
c 256	11	100.0	4699	3	US-08-649-518-1	Sequence 1, Appli	329	11	100.0	9401	3	US-08-432-693-1	Sequence 1, Appli
c 257	11	100.0	4821	3	US-08-913-374-1	Sequence 1, Appli	330	11	100.0	9416	3	US-08-811-566-19	Sequence 19, Appli
c 258	11	100.0	5009	1	US-08-487-890A-3	Sequence 3, Appli	331	11	100.0	9416	3	US-09-034-756-19	Sequence 19, Appli
c 259	11	100.0	5009	2	US-08-478-433-3	Sequence 3, Appli	332	11	100.0	9416	3	US-08-823-895A-26	Sequence 26, Appli
c 260	11	100.0	5009	2	US-08-337-483-3	Sequence 3, Appli	333	11	100.0	9416	4	US-10-104-966-13	Sequence 13, Appli
c 261	11	100.0	5009	2	US-08-478-373-3	Sequence 3, Appli	334	11	100.0	9595	3	US-09-014-416-4	Sequence 4, Appli
c 262	11	100.0	5009	3	US-08-474-671-3	Sequence 3, Appli	335	11	100.0	9599	3	US-09-014-416-2	Sequence 2, Appli
c 263	11	100.0	5009	3	US-08-483-577A-3	Sequence 3, Appli	336	11	100.0	9599	3	US-09-014-416-6	Sequence 6, Appli
c 264	11	100.0	5009	3	US-08-897-438-3	Sequence 3, Appli	337	11	100.0	9646	3	US-08-811-566-1	Sequence 1, Appli
c 265	11	100.0	5009	3	US-08-637-654-3	Sequence 3, Appli	338	11	100.0	9646	4	US-09-034-756-1	Sequence 1, Appli
c 266	11	100.0	5033	1	US-08-649-518-3	Sequence 3, Appli	339	11	100.0	10818	4	US-09-949-016-13583	Sequence 13583, A
c 267	11	100.0	5033	1	US-08-487-890A-2	Sequence 2, Appli	340	11	100.0	11076	4	US-09-539-601-1	Sequence 1, Appli
c 268	11	100.0	5033	2	US-08-478-435-2	Sequence 2, Appli	341	11	100.0	11076	4	US-09-539-601-19	Sequence 19, Appli
c 269	11	100.0	5033	2	US-08-337-483-2	Sequence 2, Appli	342	11	100.0	11076	4	US-09-539-601-25	Sequence 25, Appli
c 270	11	100.0	5033	2	US-08-478-373-2	Sequence 2, Appli	343	11	100.0	11076	4	US-09-539-601-31	Sequence 31, Appli
c 271	11	100.0	5033	3	US-08-474-671-2	Sequence 2, Appli	c 344	11	100.0	11209	4	US-09-949-016-17514	Sequence 17514, A
c 272	11	100.0	5033	3	US-08-483-577A-2	Sequence 2, Appli	c 345	11	100.0	11261	4	US-09-949-016-14358	Sequence 14358, A
c 273	11	100.0	5033	3	US-08-897-438-2	Sequence 2, Appli	c 346	11	100.0	11261	4	US-09-949-016-14908	Sequence 14908, A
c 274	11	100.0	5033	3	US-08-637-654-2	Sequence 2, Appli	c 347	11	100.0	12232	4	US-09-949-016-12570	Sequence 12570, A
c 275	11	100.0	5033	3	US-08-649-518-2	Sequence 2, Appli	348	11	100.0	12240	4	US-09-949-016-18209	Sequence 18209, A
c 276	11	100.0	5099	1	US-08-487-890A-4	Sequence 4, Appli	349	11	100.0	12980	3	US-08-811-566-5	Sequence 5, Appli
c 277	11	100.0	5099	2	US-08-478-435-4	Sequence 4, Appli	350	11	100.0	12980	3	US-09-034-756-5	Sequence 5, Appli
c 278	11	100.0	5099	2	US-08-337-483-4	Sequence 4, Appli	c 351	11	100.0	14707	4	US-09-312-762A-3	Sequence 3, Appli
c 279	11	100.0	5099	3	US-08-478-373-4	Sequence 4, Appli	c 352	11	100.0	15192	4	US-09-949-016-15143	Sequence 15143, A
c 280	11	100.0	5099	3	US-08-474-671-4	Sequence 4, Appli	c 353	11	100.0	19112	4	US-09-949-016-17541	Sequence 17541, A
c 281	11	100.0	5099	3	US-08-483-577A-4	Sequence 4, Appli	354	11	100.0	19227	4	US-09-949-016-12127	Sequence 12127, A
c 282	11	100.0	5099	3	US-08-897-438-4	Sequence 4, Appli	355	11	100.0	19228	4	US-09-949-016-16285	Sequence 16285, A
c 283	11	100.0	5099	3	US-08-637-654-4	Sequence 4, Appli	356	11	100.0	19332	2	US-08-477-451-25	Sequence 25, Appli
c 284	11	100.0	5099	3	US-08-649-518-4	Sequence 4, Appli	357	11	100.0	21862	4	US-09-949-016-17319	Sequence 17319, A
c 285	11	100.0	5125	1	US-08-453-552-11	Sequence 11, Appl	c 358	11	100.0	22281	4	US-09-949-016-14778	Sequence 14778, A
c 286	11	100.0	5125	2	US-08-710-637-11	Sequence 11, Appl	359	11	100.0	23757	4	US-09-949-016-12010	Sequence 12010, A
c 287	11	100.0	5125	5	PCT-US93-00907-11	Sequence 11, Appl	360	11	100.0	23792	4	US-09-949-016-16189	Sequence 16189, A
c 288	11	100.0	5144	1	US-08-487-890A-105	Sequence 105, App	361	11	100.0	26385	3	US-08-961-527-3	Sequence 3, Appli
c 289	11	100.0	5144	2	US-08-478-435-105	Sequence 105, App	c 362	11	100.0	31000	4	US-09-949-016-15239	Sequence 15239, A
c 290	11	100.0	5144	2	US-08-337-483-105	Sequence 105, App	c 363	11	100.0	32725	4	US-09-949-016-16586	Sequence 16586, A
c 291	11	100.0	5144	3	US-08-478-373-105	Sequence 105, App	c 364	11	100.0	35913	4	US-09-949-016-16586	Sequence 16586, A
c 292	11	100.0	5144	3	US-08-474-671-105	Sequence 105, App	c 365	11	100.0	36577	4	US-09-949-016-13176	Sequence 13176, A
c 293	11	100.0	5144	3	US-08-483-577A-105	Sequence 105, App	366	11	100.0	39489	4	US-09-949-016-13886	Sequence 13886, A
c 294	11	100.0	5144	3	US-08-897-438-105	Sequence 105, App	367	11	100.0	39686	4	US-09-949-016-13633	Sequence 13633, A
c 295	11	100.0	5144	3	US-08-637-654-105	Sequence 105, App	c 368	11	100.0	42954	4	US-09-949-016-17123	Sequence 17123, A
c 296	11	100.0	5144	3	US-08-649-518-105	Sequence 105, App	c 369	11	100.0	42954	4	US-09-949-016-17124	Sequence 17124, A
c 297	11	100.0	5199	4	US-09-949-016-5474	Sequence 5474, Ap	c 370	11	100.0	45613	4	US-09-596-002-22	Sequence 22, Appli
c 298	11	100.0	5323	2	US-08-453-552-9	Sequence 9, Appli	c 371	11	100.0	46499	4	US-09-949-016-14032	Sequence 14032, A
c 299	11	100.0	5323	2	US-08-710-637-9	Sequence 9, Appli	372	11	100.0	48313	4	US-09-949-016-17088	Sequence 17088, A
c 300	11	100.0	5323	5	PCT-US93-00907-9	Sequence 9, Appli	373	11	100.0	49487	4	US-09-949-016-11770	Sequence 11770, A
c 301	11	100.0	5475	4	US-09-543-681A-837	Sequence 837, App	374	11	100.0	52457	4	US-09-949-016-12418	Sequence 12418, A
c 302	11	100.0	5544	4	US-08-956-171E-110	Sequence 110, App	375	11	100.0	55851	4	US-09-949-016-13732	Sequence 13732, A
c 303	11	100.0	5544	4	US-08-781-986A-110	Sequence 110, App	c 376	11	100.0	57331	4	US-09-949-016-17277	Sequence 17277, A
c 304	11	100.0	5599	2	US-08-477-451-9	Sequence 9, Appli	377	11	100.0	63982	4	US-09-949-016-16769	Sequence 16769, A
c 305	11	100.0	5599	2	US-08-477-451-13	Sequence 13, Appli	378	11	100.0	65792	4	US-09-596-002-31	Sequence 31, Appli
c 306	11	100.0	5640	4	US-09-949-016-385	Sequence 385, App	379	11	100.0	66247	4	US-09-949-016-16009	Sequence 16009, A
c 307	11	100.0	5643	4	US-09-949-016-4543	Sequence 4543, Ap	380	11	100.0	66428	4	US-09-949-016-12917	Sequence 12917, A
c 308	11	100.0	5762	3	US-09-919-172-55	Sequence 55, Appli	c 381	11	100.0	68035	4	US-09-949-016-16219	Sequence 16219, A
c 309	11	100.0	6156	3	US-08-891-640-1	Sequence 1, Appli	c 382	11	100.0	80246	3	US-09-078-294-4	Sequence 4, Appli
c 310	11	100.0	6156	3	US-09-723-535-3	Sequence 3, Appli	383	11	100.0	80411	4	US-09-949-016-15777	Sequence 15777, A
c 311	11	100.0	6156	4	US-09-949-016-867	Sequence 867, App	c 384	11	100.0	80595	3	US-09-078-294-3	Sequence 3, Appli
c 312	11	100.0	7106	1	US-08-188-281B-8	Sequence 8, Appli	385	11	100.0	83697	4	US-09-949-016-16040	Sequence 16040, A
c 313	11	100.0	7106	1	US-08-453-552-5	Sequence 5, Appli	c 386	11	100.0	84761	4	US-09-949-016-11919	Sequence 11919, A
c 314	11	100.0	7106	2	US-08-710-637-5	Sequence 5, Appli	c 387	11	100.0	84763	4	US-09-949-016-13914	Sequence 13914, A
c 315	11	100.0	7106	5	PCT-US93-00907-5	Sequence 5, Appli	c 388	11	100.0	88240	4	US-09-949-016-16279	Sequence 16279, A
c 316	11	100.0	7106	5	PCT-US94-07280-8	Sequence 8, Appli	c 389	11	100.0	93689	4	US-09-949-016-13089	Sequence 13089, A
c 317	11	100.0	7106	5	PCT-US95-01087-8	Sequence 8, Appli	c 390	11	100.0	92581	4	US-09-949-016-12182	Sequence 12182, A
c 318	11	100.0	7298	1	US-08-453-552-3	Sequence 3, Appli	c 391	11	100.0	92581	4	US-09-949-016-16542	Sequence 16542, A
c 319	11	100.0	7298	2	US-08-710-637-3	Sequence 3, Appli	392	11	100.0	94095	4	US-09-949-016-14389	Sequence 14389, A

c 393	11	100.0	94750	4	US-09-596-002-38	Sequence 38, Appl	c 466	11	100.0	524032	4	US-09-949-016-16929	Sequence 16929, A
c 394	11	100.0	96987	4	US-09-949-016-14429	Sequence 14429, A	c 467	11	100.0	524032	4	US-09-949-016-16930	Sequence 16930, A
c 395	11	100.0	98844	3	US-09-791-211-10	Sequence 10, Appl	c 468	11	100.0	524032	4	US-09-949-016-16931	Sequence 16931, A
c 397	11	100.0	99629	4	US-09-596-002-37	Sequence 37, Appl	c 469	11	100.0	529885	4	US-09-949-016-14340	Sequence 14340, A
c 398	11	100.0	106929	4	US-09-949-016-12060	Sequence 12060, A	c 470	11	100.0	529885	4	US-09-949-016-14341	Sequence 14341, A
c 399	11	100.0	106929	4	US-09-949-016-16618	Sequence 16618, A	c 471	11	100.0	529885	4	US-09-949-016-14342	Sequence 14342, A
c 400	11	100.0	107329	4	US-09-949-016-12663	Sequence 12663, A	c 472	11	100.0	529885	4	US-09-949-016-14343	Sequence 14343, A
c 401	11	100.0	107329	4	US-09-949-016-12664	Sequence 12664, A	c 473	11	100.0	529885	4	US-09-949-016-14344	Sequence 14344, A
c 402	11	100.0	107330	4	US-09-949-016-15408	Sequence 15408, A	c 474	11	100.0	529885	4	US-09-949-016-14345	Sequence 14345, A
c 403	11	100.0	107330	4	US-09-949-016-15409	Sequence 15409, A	c 475	11	100.0	529885	4	US-09-949-016-14346	Sequence 14346, A
c 404	11	100.0	107330	4	US-09-949-016-15410	Sequence 15410, A	c 476	11	100.0	529885	4	US-09-949-016-14347	Sequence 14347, A
c 405	11	100.0	107330	4	US-09-949-016-15411	Sequence 15411, A	c 477	11	100.0	636591	4	US-09-949-016-11808	Sequence 11808, A
c 406	11	100.0	107751	4	US-09-949-016-12662	Sequence 12662, A	c 478	11	100.0	636591	4	US-09-949-016-11808	Sequence 11808, A
c 407	11	100.0	107751	4	US-09-949-016-15412	Sequence 15412, A	c 479	11	100.0	678533	4	US-09-949-016-14577	Sequence 14577, A
c 408	11	100.0	107751	4	US-09-949-016-15413	Sequence 15413, A	c 480	11	100.0	678533	4	US-09-949-016-14577	Sequence 14577, A
c 409	11	100.0	107751	4	US-09-949-016-15414	Sequence 15414, A	c 481	11	100.0	767677	4	US-09-949-016-12147	Sequence 12147, A
c 410	11	100.0	107925	4	US-09-949-016-15415	Sequence 15415, A	c 482	11	100.0	767677	4	US-09-949-016-12147	Sequence 12147, A
c 411	11	100.0	107925	4	US-09-949-016-11875	Sequence 11875, A	c 483	11	100.0	767677	4	US-09-949-016-12147	Sequence 12147, A
c 412	11	100.0	107926	4	US-09-949-016-15405	Sequence 15405, A	c 484	11	100.0	786431	4	US-09-949-016-17361	Sequence 17361, A
c 413	11	100.0	107926	4	US-09-949-016-15406	Sequence 15406, A	c 485	11	100.0	1830121	4	US-09-557-884-1	Sequence 1, Appl
c 414	11	100.0	107926	4	US-09-949-016-15407	Sequence 15407, A	c 486	11	100.0	1830121	4	US-09-557-884-1	Sequence 1, Appl
c 415	11	100.0	110402	4	US-09-949-016-17295	Sequence 17295, A	c 487	11	100.0	1830121	4	US-09-557-884-1	Sequence 1, Appl
c 416	11	100.0	110403	4	US-09-949-016-12741	Sequence 12741, A	c 488	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 417	11	100.0	110403	4	US-09-949-016-14196	Sequence 14196, A	c 489	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 418	11	100.0	111454	4	US-09-949-016-12737	Sequence 12737, A	c 490	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 419	11	100.0	111459	4	US-09-949-016-12737	Sequence 12737, A	c 491	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 420	11	100.0	113379	4	US-09-949-016-17561	Sequence 17561, A	c 492	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 421	11	100.0	113379	4	US-09-949-016-17562	Sequence 17562, A	c 493	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 422	11	100.0	115992	4	US-09-818-512-3	Sequence 3, Appl	c 494	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 423	11	100.0	115992	4	US-09-949-016-11844	Sequence 11844, A	c 495	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 424	11	100.0	121970	4	US-09-949-016-13606	Sequence 13606, A	c 496	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 425	11	100.0	121970	4	US-09-949-016-17216	Sequence 17216, A	c 497	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 426	11	100.0	122664	4	US-09-949-016-15794	Sequence 15794, A	c 498	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 427	11	100.0	122664	4	US-09-949-016-16396	Sequence 16396, A	c 499	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 428	11	100.0	126200	4	US-09-949-016-11824	Sequence 11824, A	c 500	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 429	11	100.0	126200	4	US-09-949-016-13193	Sequence 13193, A	c 501	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 430	11	100.0	128175	4	US-09-949-016-16268	Sequence 16268, A	c 502	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 431	11	100.0	143776	4	US-09-949-001-29	Sequence 29, Appl	c 503	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 432	11	100.0	144034	4	US-09-949-001-35	Sequence 35, Appl	c 504	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 433	11	100.0	149222	4	US-09-949-016-15890	Sequence 15890, A	c 505	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 434	11	100.0	150032	4	US-09-949-016-14321	Sequence 14321, A	c 506	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 435	11	100.0	150032	4	US-09-949-016-13042	Sequence 13042, A	c 507	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 436	11	100.0	163181	4	US-09-949-016-13730	Sequence 13730, A	c 508	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 437	11	100.0	164061	4	US-09-949-016-17422	Sequence 17422, A	c 509	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 438	11	100.0	174259	4	US-09-949-016-11968	Sequence 11968, A	c 510	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 439	11	100.0	174262	4	US-09-949-016-11968	Sequence 11968, A	c 511	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 440	11	100.0	175265	4	US-09-949-016-14259	Sequence 14259, A	c 512	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 441	11	100.0	177669	4	US-09-949-016-16089	Sequence 16089, A	c 513	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 442	11	100.0	187580	4	US-09-949-016-13713	Sequence 13713, A	c 514	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 443	11	100.0	189560	4	US-09-949-016-13266	Sequence 13266, A	c 515	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 444	11	100.0	194915	4	US-09-949-016-15584	Sequence 15584, A	c 516	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 445	11	100.0	227390	4	US-09-949-016-12201	Sequence 12201, A	c 517	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 446	11	100.0	227391	4	US-09-949-016-13665	Sequence 13665, A	c 518	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 447	11	100.0	235452	4	US-09-949-016-13675	Sequence 13675, A	c 519	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 448	11	100.0	238815	4	US-09-949-016-16274	Sequence 16274, A	c 520	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 449	11	100.0	238815	4	US-09-949-016-16274	Sequence 16274, A	c 521	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 450	11	100.0	246240	2	US-08-724-394A-20	Sequence 20, Appl	c 522	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 451	11	100.0	246240	2	US-08-724-394A-22	Sequence 22, Appl	c 523	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 452	11	100.0	247781	4	US-09-949-016-14193	Sequence 14193, A	c 524	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 453	11	100.0	255679	4	US-09-949-016-17189	Sequence 17189, A	c 525	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 454	11	100.0	256287	4	US-09-949-016-14608	Sequence 14608, A	c 526	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 455	11	100.0	269223	4	US-09-596-002-41	Sequence 41, Appl	c 527	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 456	11	100.0	343352	4	US-09-949-016-13498	Sequence 13498, A	c 528	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 457	11	100.0	363032	4	US-09-949-016-14415	Sequence 14415, A	c 529	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 458	11	100.0	363033	4	US-09-949-016-15754	Sequence 15754, A	c 530	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 459	11	100.0	373182	4	US-09-949-016-17371	Sequence 17371, A	c 531	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 460	11	100.0	373694	4	US-09-949-016-12062	Sequence 12062, A	c 532	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 461	11	100.0	422118	4	US-09-949-016-16297	Sequence 16297, A	c 533	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 462	11	100.0	422592	4	US-09-949-016-14182	Sequence 14182, A	c 534	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 463	11	100.0	462589	4	US-09-949-016-13900	Sequence 12900, A	c 535	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 464	11	100.0	476044	4	US-09-949-016-12412	Sequence 12412, A	c 536	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl
c 465	11	100.0	524032	4	US-09-949-016-16928	Sequence 16928, A	c 537	11	100.0	4403755	3	US-09-103-840A-2	Sequence 2, Appl



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541	10	90.9	201	4	US-09-248-796A-13168	Sequence 13168, A	c 614	10	90.9	444	4	US-09-270-767-6461	Sequence 6461, Ap
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553	10	90.9	282	4	US-09-248-796A-13347	Sequence 13347, A	c 626	10	90.9	457	4	US-09-736-457-685	Sequence 685, App
554	10	90.9	286	4	US-09-621-976-11456	Sequence 11456, A	c 627	10	90.9	457	4	US-09-614-124B-685	Sequence 685, App
555	10	90.9	287	4	US-09-313-294A-4492	Sequence 4492, Ap	c 628	10	90.9	457	4	US-09-671-325-685	Sequence 685, App
556	10	90.9	288	4	US-09-313-294A-920	Sequence 820, App	c 629	10	90.9	457	4	US-09-589-184-685	Sequence 685, App
557	10	90.9	288	4	US-09-313-294A-8646	Sequence 8646, Ap	c 630	10	90.9	457	4	US-09-658-824-685	Sequence 685, App
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564	10	90.9	298	4	US-09-566-076-5	Sequence 5, Appl	c 637	10	90.9	471	4	US-09-540-236-783	Sequence 783, App
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569	10	90.9	309	4	US-09-540-236-735	Sequence 735, App	c 642	10	90.9	477	4	US-09-543-681A-3282	Sequence 3282, Ap
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584	10	90.9	383	4	US-09-513-999C-35358	Sequence 35358, A	c 657	10	90.9	492	4	US-09-270-767-5511	Sequence 5511, Ap
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586	10	90.9	384	4	US-09-270-767-16214	Sequence 16214, A	c 659	10	90.9	496	4	US-09-248-796A-3327	Sequence 3327, Ap
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589	10	90.9	399	4	US-09-513-999C-10448	Sequence 10448, A	c 662	10	90.9	506	4	US-09-854-133-633	Sequence 633, App
590	10	90.9	400	4	US-08-956-171E-3323	Sequence 3323, Ap	c 663	10	90.9	509	4	US-09-621-976-1932	Sequence 1932, Ap
591	10	90.9	400	4	US-08-781-986A-3323	Sequence 3323, Ap	c 664	10	90.9	509	4	US-09-270-767-9159	Sequence 9159, Ap
592	10	90.9	409	4	US-08-956-171E-1248	Sequence 1248, Ap	c 665	10	90.9	509	4	US-09-270-767-24441	Sequence 24441, A
593	10	90.9	409	4	US-08-781-986A-1248	Sequence 1248, Ap	c 666	10	90.9	516	3	US-09-134-001C-2322	Sequence 2322, Ap
594	10	90.9	410	3	US-08-936-107A-35	Sequence 35, Appl	c 667	10	90.9	519	4	US-09-540-236-1536	Sequence 1536, Ap
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596	10	90.9	417	4	US-09-107-532A-3029	Sequence 3029, Ap	c 669	10	90.9	526	4	US-09-513-999C-90	Sequence 90, Appl
597	10	90.9	420	4	US-09-540-236-1693	Sequence 1693, Ap	c 670	10	90.9	528	4	US-09-663-751-147	Sequence 147, App
598	10	90.9	420	4	US-09-513-999C-9224	Sequence 9224, Ap	c 671	10	90.9	528	4	US-09-134-000C-972	Sequence 972, App
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610	10	90.9	442	4	US-09-621-976-7965	Sequence 7965, Ap	c 683	10	90.9	558	4	US-09-565-423-16	Sequence 16, Appl
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c 686	10	90.9	567	1	US-08-442-063A-38	Sequence 38, Appl	c 759	10	90.9	601	4	US-09-949-016-59049	Sequence 59049, A
c 687	10	90.9	573	2	US-08-290-665A-154	Sequence 154, App	c 760	10	90.9	601	4	US-09-949-016-59063	Sequence 59063, A
c 688	10	90.9	573	5	PCT-US95-10398-154	Sequence 154, App	c 761	10	90.9	601	4	US-09-949-016-59904	Sequence 59904, A
c 689	10	90.9	574	4	US-09-915-039-401	Sequence 401, App	c 762	10	90.9	601	4	US-09-949-016-61114	Sequence 61114, A
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c 692	10	90.9	587	4	US-10-012-542-123	Sequence 123, App	c 765	10	90.9	601	4	US-09-949-016-64295	Sequence 64295, A
c 693	10	90.9	587	4	US-10-115-123-123	Sequence 123, App	c 766	10	90.9	601	4	US-09-949-016-64296	Sequence 64296, A
c 694	10	90.9	594	4	US-09-252-991A-7619	Sequence 7619, Ap	c 767	10	90.9	601	4	US-09-949-016-65495	Sequence 65495, A
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c 696	10	90.9	597	4	US-09-543-681A-2594	Sequence 2594, Ap	c 769	10	90.9	601	4	US-09-949-016-67826	Sequence 67826, A
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c 700	10	90.9	601	4	US-09-949-016-19574	Sequence 19574, A	c 773	10	90.9	601	4	US-09-949-016-69361	Sequence 69361, A
c 701	10	90.9	601	4	US-09-949-016-23473	Sequence 23473, A	c 774	10	90.9	601	4	US-09-949-016-70427	Sequence 70427, A
c 702	10	90.9	601	4	US-09-949-016-23474	Sequence 23474, A	c 775	10	90.9	601	4	US-09-949-016-70428	Sequence 70428, A
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c 705	10	90.9	601	4	US-09-949-016-24224	Sequence 24224, A	c 778	10	90.9	601	4	US-09-949-016-73003	Sequence 73003, A
c 706	10	90.9	601	4	US-09-949-016-25316	Sequence 25316, A	c 779	10	90.9	601	4	US-09-949-016-73576	Sequence 73576, A
c 707	10	90.9	601	4	US-09-949-016-25317	Sequence 25317, A	c 780	10	90.9	601	4	US-09-949-016-74623	Sequence 74623, A
c 708	10	90.9	601	4	US-09-949-016-25318	Sequence 25318, A	c 781	10	90.9	601	4	US-09-949-016-74624	Sequence 74624, A
c 709	10	90.9	601	4	US-09-949-016-26021	Sequence 26021, A	c 782	10	90.9	601	4	US-09-949-016-74657	Sequence 74657, A
c 710	10	90.9	601	4	US-09-949-016-26022	Sequence 26022, A	c 783	10	90.9	601	4	US-09-949-016-75685	Sequence 75685, A
c 711	10	90.9	601	4	US-09-949-016-27343	Sequence 27343, A	c 784	10	90.9	601	4	US-09-949-016-75686	Sequence 75686, A
c 712	10	90.9	601	4	US-09-949-016-28471	Sequence 28471, A	c 785	10	90.9	601	4	US-09-949-016-75927	Sequence 75927, A
c 713	10	90.9	601	4	US-09-949-016-28472	Sequence 28472, A	c 786	10	90.9	601	4	US-09-949-016-76107	Sequence 76107, A
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c 716	10	90.9	601	4	US-09-949-016-34682	Sequence 34682, A	c 789	10	90.9	601	4	US-09-949-016-76558	Sequence 76558, A
c 717	10	90.9	601	4	US-09-949-016-34682	Sequence 34682, A	c 790	10	90.9	601	4	US-09-949-016-77808	Sequence 77808, A
c 718	10	90.9	601	4	US-09-949-016-35835	Sequence 35835, A	c 791	10	90.9	601	4	US-09-949-016-78056	Sequence 78056, A
c 719	10	90.9	601	4	US-09-949-016-35836	Sequence 35836, A	c 792	10	90.9	601	4	US-09-949-016-78056	Sequence 78056, A
c 720	10	90.9	601	4	US-09-949-016-35837	Sequence 35837, A	c 793	10	90.9	601	4	US-09-949-016-78931	Sequence 78931, A
c 721	10	90.9	601	4	US-09-949-016-35912	Sequence 35912, A	c 794	10	90.9	601	4	US-09-949-016-78932	Sequence 78932, A
c 722	10	90.9	601	4	US-09-949-016-35914	Sequence 35914, A	c 795	10	90.9	601	4	US-09-949-016-78933	Sequence 78933, A
c 723	10	90.9	601	4	US-09-949-016-35999	Sequence 35999, A	c 796	10	90.9	601	4	US-09-949-016-79555	Sequence 79555, A
c 724	10	90.9	601	4	US-09-949-016-36000	Sequence 36000, A	c 797	10	90.9	601	4	US-09-949-016-79556	Sequence 79556, A
c 725	10	90.9	601	4	US-09-949-016-36001	Sequence 36001, A	c 798	10	90.9	601	4	US-09-949-016-79557	Sequence 79557, A
c 726	10	90.9	601	4	US-09-949-016-36118	Sequence 36118, A	c 799	10	90.9	601	4	US-09-949-016-79558	Sequence 79558, A
c 727	10	90.9	601	4	US-09-949-016-36119	Sequence 36119, A	c 800	10	90.9	601	4	US-09-949-016-80054	Sequence 80054, A
c 728	10	90.9	601	4	US-09-949-016-36120	Sequence 36120, A	c 801	10	90.9	601	4	US-09-949-016-80892	Sequence 80892, A
c 729	10	90.9	601	4	US-09-949-016-36120	Sequence 36120, A	c 802	10	90.9	601	4	US-09-949-016-80893	Sequence 80893, A
c 730	10	90.9	601	4	US-09-949-016-36120	Sequence 36120, A	c 803	10	90.9	601	4	US-09-949-016-82728	Sequence 82728, A
c 731	10	90.9	601	4	US-09-949-016-38781	Sequence 38781, A	c 804	10	90.9	601	4	US-09-949-016-86620	Sequence 86620, A
c 732	10	90.9	601	4	US-09-949-016-38782	Sequence 38782, A	c 805	10	90.9	601	4	US-09-949-016-86930	Sequence 86930, A
c 733	10	90.9	601	4	US-09-949-016-38782	Sequence 38782, A	c 806	10	90.9	601	4	US-09-949-016-87180	Sequence 87180, A
c 734	10	90.9	601	4	US-09-949-016-39967	Sequence 39967, A	c 807	10	90.9	601	4	US-09-949-016-87940	Sequence 87940, A
c 735	10	90.9	601	4	US-09-949-016-40160	Sequence 40160, A	c 808	10	90.9	601	4	US-09-949-016-88581	Sequence 88581, A
c 736	10	90.9	601	4	US-09-949-016-40161	Sequence 40161, A	c 809	10	90.9	601	4	US-09-949-016-88582	Sequence 88582, A
c 737	10	90.9	601	4	US-09-949-016-40170	Sequence 40170, A	c 810	10	90.9	601	4	US-09-949-016-88583	Sequence 88583, A
c 738	10	90.9	601	4	US-09-949-016-42815	Sequence 42815, A	c 811	10	90.9	601	4	US-09-949-016-88713	Sequence 88713, A
c 739	10	90.9	601	4	US-09-949-016-44737	Sequence 44737, A	c 812	10	90.9	601	4	US-09-949-016-88963	Sequence 88963, A
c 740	10	90.9	601	4	US-09-949-016-44738	Sequence 44738, A	c 813	10	90.9	601	4	US-09-949-016-89640	Sequence 89640, A
c 741	10	90.9	601	4	US-09-949-016-44845	Sequence 44845, A	c 814	10	90.9	601	4	US-09-949-016-89641	Sequence 89641, A
c 742	10	90.9	601	4	US-09-949-016-44846	Sequence 44846, A	c 815	10	90.9	601	4	US-09-949-016-90443	Sequence 90443, A
c 743	10	90.9	601	4	US-09-949-016-44847	Sequence 44847, A	c 816	10	90.9	601	4	US-09-949-016-90531	Sequence 90531, A
c 744	10	90.9	601	4	US-09-949-016-44906	Sequence 44906, A	c 817	10	90.9	601	4	US-09-949-016-90531	Sequence 90531, A
c 745	10	90.9	601	4	US-09-949-016-47869	Sequence 47869, A	c 818	10	90.9	601	4	US-09-949-016-90619	Sequence 90619, A
c 746	10	90.9	601	4	US-09-949-016-50524	Sequence 50524, A	c 819	10	90.9	601	4	US-09-949-016-90707	Sequence 90707, A
c 747	10	90.9	601	4	US-09-949-016-50524	Sequence 50524, A	c 820	10	90.9	601	4	US-09-949-016-90795	Sequence 90795, A
c 748	10	90.9	601	4	US-09-949-016-54430	Sequence 54430, A	c 821	10	90.9	601	4	US-09-949-016-90883	Sequence 90883, A
c 749	10	90.9	601	4	US-09-949-016-54431	Sequence 54431, A	c 822	10	90.9	601	4	US-09-949-016-90971	Sequence 90971, A
c 750	10	90.9	601	4	US-09-949-016-55754	Sequence 55754, A	c 823	10	90.9	601	4	US-09-949-016-91059	Sequence 91059, A
c 751	10	90.9	601	4	US-09-949-016-56024	Sequence 56024, A	c 824	10	90.9	601	4	US-09-949-016-91630	Sequence 91630, A
c 752	10	90.9	601	4	US-09-949-016-56042	Sequence 56042, A	c 825	10	90.9	601	4	US-09-949-016-92015	Sequence 92015, A
c 753	10	90.9	601	4	US-09-949-016-56928	Sequence 56928, A	c 826	10	90.9	601	4	US-09-949-016-92016	Sequence 92016, A
c 754	10	90.9	601	4	US-09-949-016-56929	Sequence 56929, A	c 827	10	90.9	601	4	US-09-949-016-92536	Sequence 92536, A
c 755	10	90.9	601	4	US-09-949-016-57607	Sequence 57607, A	c 828	10	90.9	601	4	US-09-949-016-103477	Sequence 103477, A
c 756	10	90.9	601	4	US-09-949-016-57608	Sequence 57608, A	c 829	10	90.9	601	4	US-09-949-016-103478	Sequence 103478, A
c 757	10	90.9	601	4	US-09-949-016-57949	Sequence 57949, A	c 830	10	90.9	601	4	US-09-949-016-103479	Sequence 103479, A



977 10 90.9 601 4 US-09-949-016-184759  
978 10 90.9 601 4 US-09-949-016-184823  
979 10 90.9 601 4 US-09-949-016-184978  
c 980 10 90.9 601 4 US-09-949-016-185671  
981 10 90.9 601 4 US-09-949-016-185915  
982 10 90.9 601 4 US-09-949-016-185916  
c 983 10 90.9 601 4 US-09-949-016-190515  
c 984 10 90.9 601 4 US-09-949-016-190847  
c 985 10 90.9 601 4 US-09-949-016-190848  
c 986 10 90.9 601 4 US-09-949-016-191278  
c 987 10 90.9 601 4 US-09-949-016-191279  
c 988 10 90.9 601 4 US-09-949-016-192594  
989 10 90.9 601 4 US-09-949-016-193663  
990 10 90.9 601 4 US-09-949-016-193690  
c 991 10 90.9 601 4 US-09-949-016-194115  
992 10 90.9 601 4 US-09-949-016-195251  
993 10 90.9 601 4 US-09-949-016-195561  
994 10 90.9 601 4 US-09-949-016-195562  
995 10 90.9 601 4 US-09-949-016-197194  
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997 10 90.9 601 4 US-09-949-016-197196  
998 10 90.9 601 4 US-09-949-016-197312  
999 10 90.9 601 4 US-09-949-016-197313  
1000 10 90.9 601 4 US-09-949-016-197314

## ALIGNMENTS

## RESULT 1

US-09-396-196G-49096  
; Sequence 49096, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49096  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-49096

Query Match 100.0%; Score 11; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
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Db 9 CTTTGGCACTA 19

## RESULT 2

US-09-396-196G-106030  
; Sequence 106030, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G

Sequence 184759,  
Sequence 184823,  
Sequence 184978,  
Sequence 185671,  
Sequence 185915,  
Sequence 185916,  
Sequence 190515,  
Sequence 190847,  
Sequence 190848,  
Sequence 191278,  
Sequence 191279,  
Sequence 192594,  
Sequence 193663,  
Sequence 193690,  
Sequence 194115,  
Sequence 195251,  
Sequence 195561,  
Sequence 195562,  
Sequence 197194,  
Sequence 197195,  
Sequence 197196,  
Sequence 197312,  
Sequence 197313,  
Sequence 197314,

; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 106030  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-106030

Query Match 100.0%; Score 11; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
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Db 15 CTTTGGCACTA 25

## RESULT 3

US-09-396-196G-106031  
; Sequence 106031, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 106031  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-106031

Query Match 100.0%; Score 11; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
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Db 3 CTTTGGCACTA 13

## RESULT 4

US-09-513-999C-26159  
; Sequence 26159, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2,REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 26159  
; LENGTH: 100  
; TYPE: DNA  
; ORGANISM: Homo sapiens

## US-09-513-999C-26159

Query Match 100.0%; Score 11; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
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Db 81 CTTTGGCACTA 91

## RESULT 5

US-09-248-796A-8315/c  
; Sequence 8315, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 8315  
; LENGTH: 207  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-8315

Query Match 100.0%; Score 11; DB 4; Length 207;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||  
Db 178 CTTTGGCACTA 168

## RESULT 6

US-09-513-999C-27111  
; Sequence 27111, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 27111  
; LENGTH: 276  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 34  
; OTHER INFORMATION: m=a or c  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 122  
; OTHER INFORMATION: y=c or t  
US-09-513-999C-27111

Query Match 100.0%; Score 11; DB 4; Length 276;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
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Db 219 CTTTGGCACTA 229

## RESULT 7

US-09-270-767-26937/c  
; Sequence 26937, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26937  
; LENGTH: 305  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-26937

Query Match 100.0%; Score 11; DB 4; Length 305;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
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Db 105 CTTTGGCACTA 95

## RESULT 8

US-09-543-681A-963  
; Sequence 963, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETTON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 963  
; LENGTH: 321  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-963

Query Match 100.0%; Score 11; DB 4; Length 321;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
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Db 242 CTTTGGCACTA 252

## RESULT 9

US-09-513-999C-3625  
; Sequence 3625, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.

;; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

;; Patent No. 6783961  
 ;; FILE REFERENCE: 59.US2.REG  
 ;; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ;; CURRENT FILING DATE: 2000-02-24  
 ;; PRIOR APPLICATION NUMBER: US 60/122,487  
 ;; PRIOR FILING DATE: 1999-02-26  
 ;; NUMBER OF SEQ ID NOS: 36681  
 ;; SOFTWARE: Patent.pm  
 ;; SEQ ID NO 3625  
 ;; LENGTH: 341  
 ;; TYPE: DNA  
 ;; ORGANISM: Homo sapiens  
 ;; FEATURE:  
 ;; NAME/KEY: CDS  
 ;; LOCATION: 156..341  
 ;; FEATURE:  
 ;; NAME/KEY: misc\_feature  
 ;; LOCATION: 224  
 ;; OTHER INFORMATION: w=a or t  
 ;; FEATURE:  
 ;; NAME/KEY: misc\_feature  
 ;; LOCATION: 298  
 ;; OTHER INFORMATION: w=a or t  
 ;; FEATURE:  
 ;; NAME/KEY: misc\_feature  
 ;; LOCATION: 307  
 ;; OTHER INFORMATION: r=a or g  
 ;; FEATURE:  
 ;; NAME/KEY: UNSURE  
 ;; LOCATION: 23  
 ;; OTHER INFORMATION: Xaa=Arg or Ser  
 ;; FEATURE:  
 ;; NAME/KEY: UNSURE  
 ;; LOCATION: 48  
 ;; OTHER INFORMATION: Xaa=Phe or Tyr  
 ;; FEATURE:  
 ;; NAME/KEY: UNSURE  
 ;; LOCATION: 51  
 ;; OTHER INFORMATION: Xaa=Asp or Gly  
 US-09-513-999C-3625

Query Match 100.0%; Score 11; DB 4; Length 341;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
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 Db 130 CTTTGGCACTA 140

RESULT 10

US-09-270-767-7666  
 ;; Sequence 7666, Application US/09270767  
 ;; Patent No. 6703491  
 ;; GENERAL INFORMATION:  
 ;; APPLICANT: Homburger et al.  
 ;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ;; FILE REFERENCE: File Reference: 7326-094  
 ;; CURRENT APPLICATION NUMBER: US/09/270,767  
 ;; CURRENT FILING DATE: 1999-03-17  
 ;; NUMBER OF SEQ ID NOS: 62517  
 ;; SOFTWARE: PatentIn Ver. 2.0  
 ;; SEQ ID NO 7666  
 ;; LENGTH: 386  
 ;; TYPE: DNA  
 ;; ORGANISM: Drosophila melanogaster  
 US-09-270-767-7666

Query Match 100.0%; Score 11; DB 4; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 98 CTTTGGCACTA 108

RESULT 11

US-09-270-767-22948  
 ;; Sequence 22948, Application US/09270767  
 ;; Patent No. 6703491  
 ;; GENERAL INFORMATION:  
 ;; APPLICANT: Homburger et al.  
 ;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ;; FILE REFERENCE: File Reference: 7326-094  
 ;; CURRENT APPLICATION NUMBER: US/09/270,767  
 ;; CURRENT FILING DATE: 1999-03-17  
 ;; NUMBER OF SEQ ID NOS: 62517  
 ;; SOFTWARE: PatentIn Ver. 2.0  
 ;; SEQ ID NO 22948  
 ;; LENGTH: 386  
 ;; TYPE: DNA  
 ;; ORGANISM: Drosophila melanogaster  
 US-09-270-767-22948

Query Match 100.0%; Score 11; DB 4; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 98 CTTTGGCACTA 108

RESULT 12

US-09-640-173-30  
 ;; Sequence 30, Application US/09640173  
 ;; Patent No. 6613515  
 ;; GENERAL INFORMATION:  
 ;; APPLICANT: Xu, Jiangchun  
 ;; APPLICANT: Stolk, John A.  
 ;; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND  
 ;; METHODS OF USE THEREFOR  
 ;; FILE REFERENCE: 210121.484C2  
 ;; CURRENT APPLICATION NUMBER: US/09/640,173  
 ;; CURRENT FILING DATE: 2000-08-15  
 ;; NUMBER OF SEQ ID NOS: 196  
 ;; SOFTWARE: FastSeq for Windows Version 3.0  
 ;; SEQ ID NO 30  
 ;; LENGTH: 396  
 ;; TYPE: DNA  
 ;; ORGANISM: Homo sapien  
 ;; FEATURE:  
 ;; NAME/KEY: misc\_feature  
 ;; LOCATION: (1)...(396)  
 ;; OTHER INFORMATION: n = A,T,C or G  
 US-09-640-173-30

Query Match 100.0%; Score 11; DB 4; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 316 CTTTGGCACTA 326

RESULT 13

US-09-713-550-30  
 ;; Sequence 30, Application US/09713550  
 ;; Patent No. 6617109  
 ;; GENERAL INFORMATION:  
 ;; APPLICANT: Xu, Jiangchun  
 ;; APPLICANT: Stolk, John A.  
 ;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE



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; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-30

Query Match          100.0%; Score 11; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
   |||||
Db 316 CTTTGGCACTA 326

RESULT 14
US-09-825-294-30
; Sequence 30, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stoik, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-30

Query Match          100.0%; Score 11; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
   |||||
Db 316 CTTTGGCACTA 326

RESULT 15
US-09-970-966-30
; Sequence 30, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stoik, John A.
; APPLICANT: Moleseh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
```

```
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 28, 83, 126, 138, 254, 275, 298, 310, 311, 353, 363, 374,
; LOCATION: 379, 393
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-30

Query Match          100.0%; Score 11; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
   |||||
Db 316 CTTTGGCACTA 326

RESULT 16
US-09-621-976-17465/c
; Sequence 17465, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17465
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 422
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-17465

Query Match          100.0%; Score 11; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
   |||||
Db 274 CTTTGGCACTA 264

RESULT 17
US-09-621-976-2058/c
; Sequence 2058, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2058
; LENGTH: 475
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..312
; NAME/KEY: sig_peptide
; LOCATION: 88..198
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.5
; OTHER INFORMATION: seq PFFFSKLLPVFS/MM
US-09-621-976-2058

Query Match          100.0%; Score 11; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 353 CTTTGGCACTA 343

RESULT 18
US-09-248-796A-2902/c
; Sequence 2902, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2902
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2902

Query Match          100.0%; Score 11; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 160 CTTTGGCACTA 150

RESULT 19
US-09-621-976-15675/c
; Sequence 15675, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15675
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15675

Query Match          100.0%; Score 11; DB 4; Length 505;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 182 CTTTGGCACTA 172

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 170 CTTTGGCACTA 160

RESULT 20
US-09-647-224A-21/c
; Sequence 21, Application US/09647224A
; Patent No. 6482631
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Gutteridge, Steven
; APPLICANT: Hitz, William D.
; APPLICANT: Maxwell, Carl A.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tao, Yong
; APPLICANT: Vollmer, Steven J.
; TITLE OF INVENTION: TRYPTOPHAN BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB-1150-A
; CURRENT APPLICATION NUMBER: US/09/647,224A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/079,386
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/06046
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (414)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (445)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (464)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (494)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (508)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (522)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (549)
; OTHER INFORMATION: n = a, c, t, or g
; OTHER INFORMATION: n = a, c, t, or g
US-09-647-224A-21

Query Match          100.0%; Score 11; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 182 CTTTGGCACTA 172
```

```
RESULT 21
US-09-134-000C-1129
; Sequence 1129, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1129
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1129

Query Match      100.0%; Score 11; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
Db      435 CTTTGGCACTA 445

RESULT 22
US-09-517-790-3/c
; Sequence 3, Application US/09517790
; Patent No. 6544512
; GENERAL INFORMATION:
; APPLICANT: White, Jr., James F
; TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of Fu
; FILE REFERENCE: RU-0093
; CURRENT APPLICATION NUMBER: US/09/517,790
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/123,099
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Ampelomyces quisqualis
US-09-517-790-3

Query Match      100.0%; Score 11; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
Db      524 CTTTGGCACTA 514

RESULT 23
US-09-640-211A-264/c
; Sequence 264, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
```

```
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-264

Query Match      100.0%; Score 11; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
Db      187 CTTTGGCACTA 177

RESULT 24
US-09-949-016-20441
; Sequence 20441, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20441
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-20441

Query Match      100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
Db      553 CTTTGGCACTA 563

RESULT 25
US-09-949-016-20442
; Sequence 20442, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20442
; LENGTH: 601
```

; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-20442

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 549 CTTTGGCACTA 559

## RESULT 26

US-09-949-016-23566/c  
; Sequence 23566, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23566  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-23566

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 540 CTTTGGCACTA 530

## RESULT 27

US-09-949-016-25590/c  
; Sequence 25590, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25590  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-25590

Query Match 100.0%; Score 11; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 88 CTTTGGCACTA 78

## RESULT 28

US-09-949-016-29497/c  
; Sequence 29497, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29497  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-29497

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 484 CTTTGGCACTA 474

## RESULT 29

US-09-949-016-35684  
; Sequence 35684, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35684  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-35684

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 553 CTTTGGCACTA 563

## RESULT 30

US-09-949-016-35685  
; Sequence 35685, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35685  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-35685

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

Db 549 CTTTGGCACTA 559

## RESULT 31

US-09-949-016-35718  
; Sequence 35718, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35718  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-35718

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

Db 553 CTTTGGCACTA 563

## RESULT 32

US-09-949-016-35719

; Sequence 35719, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35719  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-35719

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

Db 549 CTTTGGCACTA 559

## RESULT 33

US-09-949-016-35752  
; Sequence 35752, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35752  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-35752

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

Db 553 CTTTGGCACTA 563

## RESULT 34

US-09-949-016-35753  
; Sequence 35753, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35753  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-35753

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 549 CTTTGGCACTA 559

RESULT 35  
US-09-949-016-36869  
; Sequence 36869, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36869  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-36869

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 177 CTTTGGCACTA 187

RESULT 36  
US-09-949-016-45724/c  
; Sequence 45724, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45724  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-45724

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 63 CTTTGGCACTA 53

RESULT 37  
US-09-949-016-49633/c  
; Sequence 49633, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49633  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-49633

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 504 CTTTGGCACTA 494

RESULT 38  
US-09-949-016-49634/c  
; Sequence 49634, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08



; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49634  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-49634

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||

DB 331 CTTTGGCACTA 321

## RESULT 39

US-09-949-016-56559  
; Sequence 56559, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56559  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-56559

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||

DB 260 CTTTGGCACTA 270

## RESULT 40

US-09-949-016-60165/c  
; Sequence 60165, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60165  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-60165

; ORGANISM: Human  
US-09-949-016-60165

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||

DB 329 CTTTGGCACTA 319

## RESULT 41

US-09-949-016-60166/c  
; Sequence 60166, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 60166  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-60166

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||

DB 337 CTTTGGCACTA 327

## RESULT 42

US-09-949-016-66919  
; Sequence 66919, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66919  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-66919

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
Db 138 CTTTGGCACTA 148

RESULT 43  
US-09-949-016-66920  
; Sequence 66920, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66920  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-66920

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
Db 31 CTTTGGCACTA 41

RESULT 44  
US-09-949-016-67654  
; Sequence 67654, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67654  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-67654

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
Db 215 CTTTGGCACTA 225

RESULT 45  
US-09-949-016-67726  
; Sequence 67726, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67726  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-67726

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
Db 322 CTTTGGCACTA 332

RESULT 46  
US-09-949-016-78261  
; Sequence 78261, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 78261  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-78261

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
Db 177 CTTTGGCACTA 187

RESULT 47  
US-09-949-016-86386/c  
; Sequence 86386, Application US/09949016

; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86386  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-86386

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 367 CTTTGGCACTA 357

RESULT 48  
US-09-949-016-86773/c  
; Sequence 86773, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86773  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-86773

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 481 CTTTGGCACTA 471

RESULT 49  
US-09-949-016-87066/c  
; Sequence 87066, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 87066  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-87066

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 484 CTTTGGCACTA 474

RESULT 50  
US-09-949-016-88660/c  
; Sequence 88660, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88660  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-88660

Query Match 100.0%; Score 11; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 229 CTTTGGCACTA 219

Search completed: March 12, 2005, 10:59:14  
Job time : 111 secs

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OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 08:28:43 ; Search time 1733 Seconds  
(without alignments)  
241.608 Million cell updates/sec

Title: US-10-070-588A-112

Perfect score: 11

Sequence: 1 ctttggcacta 11

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	43	8	AZ636663 1M0495D12
2	11	100.0	68	7	C0866272 Mdfst3046
3	11	100.0	72	7	T77835 ydl6c08.e1
4	11	100.0	87	9	CG668957
5	11	100.0	88	1	A1631958
6	11	100.0	88	8	BZ662266
7	11	100.0	91	4	BG409256
8	11	100.0	106	2	BE165421
9	11	100.0	107	7	CF776000
10	11	100.0	113	8	A2517183
11	11	100.0	116	4	B1130927
12	11	100.0	120	2	BF901301
13	11	100.0	120	2	AW551508
14	11	100.0	120	7	CK105615
15	11	100.0	121	2	BF352764
16	11	100.0	122	8	A2759838
17	11	100.0	127	6	CA345114
18	11	100.0	129	6	CB352552
19	11	100.0	130	9	CG918048
20	11	100.0	138	1	AA508728
21	11	100.0	138	2	BF545856
22	11	100.0	140	8	BH055493
23	11	100.0	141	1	A1965679
24	11	100.0	146	1	AA717598

c	25	11	100.0	147	9	CC516068
	26	11	100.0	149	4	BM113996
	27	11	100.0	149	4	BM405670
c	28	11	100.0	150	7	R57383
	29	11	100.0	152	7	CV071926
c	30	11	100.0	153	7	CO321951
	31	11	100.0	155	7	CO331019
	32	11	100.0	156	6	CD054495
c	33	11	100.0	156	8	BZ654414
	34	11	100.0	159	1	AV013351
c	35	11	100.0	162	5	BP671035
	36	11	100.0	162	5	BP671035
	37	11	100.0	164	5	BM485387
	38	11	100.0	168	8	BZ654404
c	39	11	100.0	168	9	CL954906
	40	11	100.0	172	9	CG869416
c	41	11	100.0	174	5	BQ294074
	42	11	100.0	175	5	BQ080480
c	43	11	100.0	177	8	AZ113246
c	44	11	100.0	178	1	AA065630
c	45	11	100.0	178	4	BM829109
c	46	11	100.0	178	5	BM406539
	47	11	100.0	180	9	CE643587
	48	11	100.0	181	4	BM110364
	49	11	100.0	181	7	CF206632
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301	11	100.0	293	8	AZ481548	AZ481548	AZ481548	374	11	100.0	310	2	BE787745	BE787745
302	11	100.0	293	8	AZ833972	AZ833972	AZ833972	375	11	100.0	310	4	BG095930	BG095930
303	11	100.0	294	1	AA666240	AA666240	AA666240	376	11	100.0	310	4	BG190695	BG190695
304	11	100.0	294	2	BB568807	BB568807	BB568807	377	11	100.0	310	4	BG193275	BG193275
305	11	100.0	294	5	BY354096	BY354096	BY354096	378	11	100.0	310	4	BG209794	BG209794
306	11	100.0	294	9	CG407725	CG407725	CG407725	379	11	100.0	310	5	BU097041	BU097041
307	11	100.0	295	2	AW325791	AW325791	AW325791	380	11	100.0	310	6	C63255	C63255
308	11	100.0	295	4	EG057076	EG057076	EG057076	381	11	100.0	310	7	CV364836	CV364836
309	11	100.0	296	2	AW145136	AW145136	AW145136	382	11	100.0	310	9	CL208080	CL208080
310	11	100.0	296	2	AW173457	AW173457	AW173457	383	11	100.0	310	9	CL430772	CL430772
311	11	100.0	296	4	BG191690	BG191690	BG191690	384	11	100.0	311	2	BF530312	BF530312
312	11	100.0	296	9	CG679592	CG679592	CG679592	385	11	100.0	311	2	AW002671	AW002671
313	11	100.0	297	1	AA908563	AA908563	AA908563	386	11	100.0	311	2	BB166148	BB166148
314	11	100.0	297	2	AW360224	AW360224	AW360224	387	11	100.0	311	5	BX639731	BX639731
315	11	100.0	297	4	BG214010	BG214010	BG214010	388	11	100.0	311	9	CL634772	CL634772
316	11	100.0	297	4	BF469782	BF469782	BF469782	389	11	100.0	312	1	AA652533	AA652533

390	11	100.0	312	2	BF737539	CM4-KT003	C 463	11	100.0	323	5	BM979499	UI-CF-DU1
391	11	100.0	312	2	AM449138	UI-H-BI3-	464	11	100.0	323	6	CB177752	in95905.x
C 392	11	100.0	312	2	BI120310	FO13P35Y	465	11	100.0	323	9	CG855019	ZMMBBc022
393	11	100.0	312	6	CB176560	PI23G01.Y	C 466	11	100.0	324	1	AU057416	AU057416
C 394	11	100.0	313	1	AA907440	A0102f10.s	C 467	11	100.0	324	1	AU057829	AU057829
C 395	11	100.0	313	2	BB507275	BB507275	468	11	100.0	324	1	AA278991	z80e003.r
C 396	11	100.0	313	4	BG214014	RST33640	469	11	100.0	324	4	BK406478	sac32g11.
397	11	100.0	313	7	CV402237	QV4-SN002	470	11	100.0	324	7	CG345926	L0533F04-
398	11	100.0	313	8	AQ971209	RPCI-23-3	C 471	11	100.0	325	1	AA672787	vs38d07.r
C 399	11	100.0	314	1	AV259425	AV259425	472	11	100.0	325	1	AI493365	tg70g08.x
C 400	11	100.0	314	1	AV524633	AV524633	C 473	11	100.0	325	1	AV307357	AV307357
C 401	11	100.0	314	2	BF787747	601482314	C 474	11	100.0	325	2	BE923133	ES7426902
C 402	11	100.0	314	4	BF985447	QV4-GN014	475	11	100.0	325	4	BG146473	maB91f04.
403	11	100.0	314	6	CA929078	MTU2CA.P1	476	11	100.0	325	7	CK767183	naQ03-1cs
404	11	100.0	314	8	BZ533613	OGAKI67TM	C 477	11	100.0	325	8	AQ843287	nbxb0007C
405	11	100.0	315	2	BB122148	BB122148	C 478	11	100.0	326	1	AA277874	va80g2.r
C 406	11	100.0	315	2	BE503891	h235b06.x	479	11	100.0	326	8	AZ385162	IMO143F03
C 407	11	100.0	315	9	CL394030	ZMMBBb024	C 480	11	100.0	326	8	BZ675902	PUBEN43TD
C 408	11	100.0	316	1	AI673589	we76b07.x	481	11	100.0	327	2	BB122890	BB122890
C 409	11	100.0	316	4	BG146261	maB73e07.	C 482	11	100.0	327	2	BF062105	7k72a08.x
C 410	11	100.0	316	4	BG210824	RST30372	C 483	11	100.0	327	7	CK319294	X9P09b06
411	11	100.0	316	6	CD911508	G550.111F	484	11	100.0	327	7	CO867115	Mxdb5906h
C 412	11	100.0	316	7	CK687116	ZF101-P00	485	11	100.0	327	7	CO994343	UMC-pd12
413	11	100.0	316	7	CK779785	UMC-bend	486	11	100.0	328	2	BZ287023	SALU_0203
C 414	11	100.0	316	7	CN776275	tae79c07-	C 487	11	100.0	328	2	BF226483	uz51e12.x
415	11	100.0	317	2	AW132076	xe72b01.x	C 488	11	100.0	328	2	BE933891	RCO-HT090
416	11	100.0	317	2	BG207041	BB207041	C 489	11	100.0	328	5	BP601545	BP601545
C 417	11	100.0	317	2	BG205712	RST25029	C 490	11	100.0	328	9	CG690277	ZMMBBc013
418	11	100.0	317	4	BG360949	gb42b10.Y	491	11	100.0	329	5	BQ495197	BQ495197
419	11	100.0	317	4	B1216362	RE23479.5	C 492	11	100.0	329	5	BQ761681	EBEm10.SQ
420	11	100.0	317	6	CA772796	ik63d03.x	C 493	11	100.0	329	5	BY518786	BY518786
421	11	100.0	317	7	CO728900	UMC-bend	C 494	11	100.0	329	7	CN942645	010921AVB
C 422	11	100.0	317	8	AZ257430	RPCI-23-1	C 495	11	100.0	330	2	BE954594	UI-M-CC1-
C 423	11	100.0	317	9	CC813094	ZMMBBc048	496	11	100.0	330	5	EX869232	EX869232
C 424	11	100.0	318	1	AV021902	AV021902	C 497	11	100.0	330	5	BY519713	BY519713
425	11	100.0	318	2	BB530435	BB530435	498	11	100.0	330	6	CA535472	C0319A02-
C 426	11	100.0	318	4	B1119675	F003P36Y	499	11	100.0	330	7	CV230514	WS01916.B
C 427	11	100.0	319	1	AT395948	AT395948	C 500	11	100.0	330	8	AQ584397	RPCI-11-4
C 428	11	100.0	319	1	AA606812	vm90h11.r	501	11	100.0	330	9	CE655262	tigr-g8s-
429	11	100.0	319	2	BB097330	BB097330	C 502	11	100.0	331	1	AI811566	wg2g11.x
430	11	100.0	319	2	BB530437	BB530437	C 503	11	100.0	331	4	BG193784	RG193784
C 431	11	100.0	319	4	BG214013	RST33639	C 504	11	100.0	331	6	CB641164	OSUNEa18B
C 432	11	100.0	319	4	BM226235	K0224G09-	505	11	100.0	331	7	CK899267	SGP162856
C 433	11	100.0	319	9	CG887622	ZMMBBb036	506	11	100.0	331	8	AQ366205	nbxb0065M
C 434	11	100.0	319	9	CL398797	ZMMBBb040	C 507	11	100.0	331	9	BX222270	Danio rer
435	11	100.0	320	1	AA954082	on62g10.s	C 508	11	100.0	332	1	AA667156	vg89d10.r
436	11	100.0	320	1	AI205735	qg32c01.x	509	11	100.0	332	1	AI051099	OW38e03.s
437	11	100.0	320	1	AI559401	tq33b09.x	510	11	100.0	332	1	AI121373	uc31g02.r
438	11	100.0	320	1	AI824623	wc19h05.x	511	11	100.0	332	2	BF226970	uz18h05.x
439	11	100.0	320	1	AL369106	McBA28H09	512	11	100.0	332	4	BG199910	RST19206
440	11	100.0	320	2	AW768667	hl51c09.x	C 513	11	100.0	332	5	EX629427	BX629427
C 441	11	100.0	320	2	BB167567	BB167567	C 514	11	100.0	332	5	EX670396	EX670396
C 442	11	100.0	320	4	BI189795	W35436 129	C 515	11	100.0	332	8	AY557359	BY557359
C 443	11	100.0	320	7	W35436	129 Moube V	516	11	100.0	333	6	BY557359	BY557359
C 444	11	100.0	320	8	AQ425575	CITBI-E1-	C 517	11	100.0	333	6	CD632309	55123210J
C 445	11	100.0	320	8	AO544643	CITBI-E1-	518	11	100.0	333	7	CO591563	DG3-51922
C 446	11	100.0	321	1	AJ686528	AJ686528	C 519	11	100.0	333	8	BH290157	CH230-207
C 447	11	100.0	321	2	BF840294	RC3-HT023	C 520	11	100.0	333	8	BH290157	CH230-207
C 448	11	100.0	321	4	BG209795	RST29322	C 521	11	100.0	334	1	AI991901	wa42b06.x
449	11	100.0	321	6	CD674760	fs14d06.Y	C 522	11	100.0	334	1	AV737315	AV737315
450	11	100.0	321	9	CNS0002V	Arabi0dp8	C 523	11	100.0	334	7	CV081603	RG204511
C 451	11	100.0	322	1	AA981813	ua31h11.r	C 524	11	100.0	334	7	CV083639	Mdft3072
C 452	11	100.0	322	1	AV303979	AV303979	C 525	11	100.0	334	9	CL572176	OB_Ba001
C 453	11	100.0	322	2	BE327051	hw06d06.x	526	11	100.0	335	2	AW192189	x1B1C04.x
454	11	100.0	322	2	BF148524	uy82d02.x	527	11	100.0	335	2	AW501859	UI-HF-B00
C 455	11	100.0	322	5	BM579721	BM579721	528	11	100.0	335	5	BQ030573	UI-1-BA0-
C 456	11	100.0	322	8	AZ760771	1M0554B13	C 529	11	100.0	335	6	CB102723	MMV_SQ013
C 457	11	100.0	322	8	AZ870193	2M0182P01	530	11	100.0	335	7	CK694433	CK694433
C 458	11	100.0	322	9	CG391423	ZMMBBc057	531	11	100.0	335	9	CG763261	ZF101-P00
459	11	100.0	323	1	AA846030	ak79b03.s	C 532	11	100.0	336	1	AV259568	ZMMBBc020
460	11	100.0	323	1	AA188850	zp79d08.r	533	11	100.0	336	2	AW347865	AV259568
461	11	100.0	323	2	BB140143	BB140143	C 534	11	100.0	336	2	BE549844	32157 MAR
462	11	100.0	323	4	BI276625	UI-R-CX0-	C 535	11	100.0	336	5	BY517671	7a20d07.x

536	11	100.0	336	7	CN866896	001026AAN	C 609	11	100.0	349	1	AI243294	AI243294	qh35h12.x
537	11	100.0	336	8	AZ838754	2M0134P08	610	11	100.0	349	1	AI895627	EST265070	
538	11	100.0	337	1	AL750352	AL750352	611	11	100.0	349	1	AA514907	nh72c02.8	
539	11	100.0	337	4	BG207686	RST27169	612	11	100.0	349	2	AW268388	xv50907.x	
540	11	100.0	337	4	BI119747	F004P56Y	613	11	100.0	349	5	BW072143	BW072143	
541	11	100.0	337	5	BQ497015	BQ497015	614	11	100.0	349	6	CD580687	CD580687	
542	11	100.0	337	5	BY519074	BY519074	615	11	100.0	349	7	CN999186	CN999186	
543	11	100.0	337	7	CF615600	CES013958	616	11	100.0	349	7	CO483057	CO483057	
544	11	100.0	337	7	CV368378	PM2-CT080	617	11	100.0	349	7	CQ937021	CQ937021	
545	11	100.0	337	7	TE63065	Yb98e08.r1	618	11	100.0	350	1	AA453089	AA453089	
546	11	100.0	337	8	BH106357	RPC1-24-3	619	11	100.0	350	2	BF733517	BF733517	
547	11	100.0	337	9	CL890389	abg02h07.	620	11	100.0	350	2	AW628002	AW628002	
548	11	100.0	338	1	AI141691	ot08e01.x	621	11	100.0	350	7	CN867652	CN867652	
549	11	100.0	338	1	AA277097	vc06h05.r	622	11	100.0	351	1	AI183068	AI183068	
550	11	100.0	338	7	CV500994	65479.1 M	623	11	100.0	351	2	BF591296	BF591296	
551	11	100.0	338	9	CL317157	CL317157	624	11	100.0	351	4	BM117843	BM117843	
552	11	100.0	339	1	AA689502	ns66h06.8	625	11	100.0	351	5	BY413554	BY413554	
553	11	100.0	339	1	AA223730	AA223730	626	11	100.0	351	6	CB867750	CB867750	
554	11	100.0	339	1	AA514256	AA514256	627	11	100.0	352	1	AI156011	AI156011	
555	11	100.0	339	2	BF171785	BF171785	628	11	100.0	352	1	AI410077	AI410077	
556	11	100.0	339	7	D66851	CELK124F1R	629	11	100.0	352	4	BM840085	BM840085	
557	11	100.0	340	2	AW474294	xs24d09.x	630	11	100.0	352	5	BQ565673	BQ565673	
558	11	100.0	340	5	BY103527	BY103527	631	11	100.0	352	5	HU158393	HU158393	
559	11	100.0	340	7	CO941320	CO941320	632	11	100.0	352	7	CN999200	CN999200	
560	11	100.0	341	2	BE185420	IL5-HT073	633	11	100.0	352	7	CO955760	CO955760	
561	11	100.0	341	4	BM150979	TCBAP1D13	634	11	100.0	352	7	CO989217	CO989217	
562	11	100.0	341	5	BP655258	BP655258	635	11	100.0	353	1	AI287981	AI287981	
563	11	100.0	341	5	BY398234	BY398234	636	11	100.0	353	1	AI311564	AI311564	
564	11	100.0	342	1	AI219361	AI219361	637	11	100.0	353	1	AV815300	AV815300	
565	11	100.0	342	6	CA535165	CA535165	638	11	100.0	353	2	AW264770	AW264770	
566	11	100.0	342	6	CD979936	CD979936	639	11	100.0	353	2	BE629131	BE629131	
567	11	100.0	342	9	CG980389	CG980389	640	11	100.0	353	5	BY428076	BY428076	
568	11	100.0	343	2	AA834096	AA834096	641	11	100.0	353	6	CB605588	CB605588	
569	11	100.0	343	2	BB138465	BB138465	642	11	100.0	353	6	CB605588	CB605588	
570	11	100.0	343	7	CO243937	CO243937	643	11	100.0	353	7	T27835	T27835	
571	11	100.0	343	7	CO661048	CO661048	644	11	100.0	353	9	CG022826	CG022826	
572	11	100.0	343	7	D64663	D64663	645	11	100.0	353	9	CL456962	CL456962	
573	11	100.0	343	8	AZ252540	AZ252540	646	11	100.0	354	1	AA4790119	AA4790119	
574	11	100.0	343	9	AG218089	AG218089	647	11	100.0	354	1	AA457594	AA457594	
575	11	100.0	343	9	CL732705	CL732705	648	11	100.0	354	2	BF703779	BF703779	
576	11	100.0	344	4	BI466431	BI466431	649	11	100.0	354	4	BI371178	BI371178	
577	11	100.0	344	7	CK515073	CK515073	650	11	100.0	354	4	BM759166	BM759166	
578	11	100.0	344	7	CO754389	CO754389	651	11	100.0	354	5	BQ309661	BQ309661	
579	11	100.0	345	1	AA776620	AA776620	652	11	100.0	354	9	CL671815	CL671815	
580	11	100.0	345	2	BP805045	BP805045	653	11	100.0	355	1	AI559892	AI559892	
581	11	100.0	345	2	AW110959	AW110959	654	11	100.0	355	1	EG239690	EG239690	
582	11	100.0	345	2	AW594752	AW594752	655	11	100.0	355	5	BY038159	BY038159	
583	11	100.0	345	4	BI164629	BI164629	656	11	100.0	355	6	CO2608	CO2608	
584	11	100.0	345	4	BM663979	BM663979	657	11	100.0	356	1	AI165825	AI165825	
585	11	100.0	345	5	BU733752	BU733752	658	11	100.0	356	2	BE173118	BE173118	
586	11	100.0	345	6	CD987618	CD987618	659	11	100.0	356	2	BE220055	BE220055	
587	11	100.0	345	7	L26621	L26621	660	11	100.0	356	4	BM144216	BM144216	
588	11	100.0	345	7	N34540	N34540	661	11	100.0	356	4	BM768330	BM768330	
589	11	100.0	346	1	AA840171	AA840171	662	11	100.0	356	6	CB117220	CB117220	
590	11	100.0	346	1	AA130363	AA130363	663	11	100.0	356	6	CB389607	CB389607	
591	11	100.0	346	1	AI686769	AI686769	664	11	100.0	356	7	CK272538	CK272538	
592	11	100.0	346	1	AI689597	AI689597	665	11	100.0	357	1	AA578557	AA578557	
593	11	100.0	346	5	BY010449	BY010449	666	11	100.0	357	1	AA549517	AA549517	
594	11	100.0	346	6	BY561340	BY561340	667	11	100.0	357	2	AW093992	AW093992	
595	11	100.0	346	6	CA949078	CA949078	668	11	100.0	357	5	BP630306	BP630306	
596	11	100.0	347	1	AA921911	AA921911	669	11	100.0	357	6	BQ212196	BQ212196	
597	11	100.0	347	1	AA921343	AA921343	670	11	100.0	357	6	CA947662	CA947662	
598	11	100.0	347	1	AA418953	AA418953	671	11	100.0	357	6	CB069604	CB069604	
599	11	100.0	347	6	CD645320	CD645320	672	11	100.0	357	6	CR697518	CR697518	
600	11	100.0	347	7	T30098	T30098	673	11	100.0	357	7	CR697518	CR697518	
601	11	100.0	347	7	AG202257	AG202257	674	11	100.0	357	7	CR697518	CR697518	
602	11	100.0	348	2	AW164169	AW164169	675	11	100.0	357	8	CA947662	CA947662	
603	11	100.0	348	4	BG056959	BG056959	676	11	100.0	358	1	AA747253	AA747253	
604	11	100.0	348	4	BG191185	BG191185	677	11	100.0	358	1	AA879413	AA879413	
605	11	100.0	348	4	BG293335	BG293335	678	11	100.0	358	1	AI360733	AI360733	
606	11	100.0	348	4	BG293335	BG293335	679	11	100.0	358	1	AI524369	AI524369	
607	11	100.0	348	7	N77558	N77558	680	11	100.0	358	1	AA426976	AA426976	
608	11	100.0	348	7	N77558	N77558	681	11	100.0	358	1	AA426976	AA426976	

682	11	100.0	358	2	BF448748	BF448748	nae32e12.	c 755	11	100.0	366	6	CD786494	CD786494	EST657855
683	11	100.0	358	5	BY507067	BY507067	BY507067	756	11	100.0	366	7	N34562	N34562	YY14F02.s1
c 684	11	100.0	358	7	CO727245	CO727245	UMC-bend	c 757	11	100.0	366	8	B34218	B34218	HS-1024-A1-
c 685	11	100.0	358	7	CO948572	CO948572	UMC-p8mm4	758	11	100.0	366	9	CL379221	CL379221	RPC144.42
c 686	11	100.0	358	9	CR317294	CR317294	Medicago	c 759	11	100.0	367	1	AI288970	AI288970	ql86e01.x
c 687	11	100.0	359	1	AA689225	AA689225	ns66h06.r	c 760	11	100.0	367	1	AV522656	AV522656	AV522656
c 688	11	100.0	359	2	AW550545	AW550545	L0066A08-	761	11	100.0	367	2	BF438247	BF438247	7Q01902.x
c 689	11	100.0	359	4	B1432620	B1432620	EST535381	c 762	11	100.0	367	4	BJ261968	BJ261968	BJ261968
c 690	11	100.0	359	5	BU762451	BU762451	sae27e02.	763	11	100.0	367	5	BU741317	BU741317	UI-E-EU0-
c 691	11	100.0	359	5	BY398282	BY398282	BY398282	764	11	100.0	367	5	BY664805	BY664805	BY664805
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c 694	11	100.0	359	7	CO997298	CO997298	CS802-3ms	767	11	100.0	367	9	CG397771	CG397771	ZMWBB001
c 695	11	100.0	360	1	AU097859	AU097859	AU097859	c 768	11	100.0	367	9	AA693943	AA693943	Z153C02.s
c 696	11	100.0	360	1	AV192100	AV192100	AV192100	c 769	11	100.0	368	1	AA693943	AA693943	Z153C02.s
c 697	11	100.0	360	1	AV203024	AV203024	AV203024	770	11	100.0	368	2	AW575059	AW575059	UI-HF-BK0
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c 699	11	100.0	360	1	AA598495	AA598495	ae38g09.s	772	11	100.0	368	4	BM034710	BM034710	hu34g06.y
c 700	11	100.0	360	4	BM197377	BM197377	CO349B04-	773	11	100.0	368	4	BM034710	BM034710	hu34g06.y
c 701	11	100.0	360	6	CS5702	CS5702	CS5702	774	11	100.0	368	5	BU700120	BU700120	UI-M-DJ0-
c 702	11	100.0	360	7	D37271	D37271	CKL043B3F	c 775	11	100.0	368	5	BY396584	BY396584	BY396584
c 703	11	100.0	360	7	R34508	R34508	Y958a04.r1	c 776	11	100.0	368	5	BY411262	BY411262	BY411262
c 704	11	100.0	360	8	BM305687	BM305687	CH230-371	c 777	11	100.0	368	7	CK682398	CK682398	ZF101-P00
c 705	11	100.0	360	9	CC785048	CC785048	ZMWBBb015	778	11	100.0	368	9	CNS00Q15	CNS00Q15	Arabi1dops
c 706	11	100.0	361	1	AI753147	AI753147	CR05h09.x	779	11	100.0	369	1	AI263477	AI263477	qi07d07.x
c 707	11	100.0	361	2	BF197901	BF197901	7p86a08.x	780	11	100.0	369	1	AA581274	AA581274	nd38f12.s
c 708	11	100.0	361	4	BI465786	BI465786	ie20a06.x	c 781	11	100.0	369	2	BB813790	BB813790	BB813790
c 709	11	100.0	361	5	BF084926	BF084926	BP084926	782	11	100.0	369	4	BM117456	BM117456	L0851H08-
c 710	11	100.0	361	5	BP085300	BP085300	BP085300	c 783	11	100.0	369	5	BQ497016	BQ497016	ES106245
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c 713	11	100.0	361	7	CO380580	CO380580	FR010010P	786	11	100.0	370	1	AA665710	AA665710	ag53h07.s
c 714	11	100.0	361	8	AQ927372	AQ927372	RPC1-23-2	787	11	100.0	370	1	AA233167	AA233167	ag53h07.s
c 715	11	100.0	362	1	AI077790	AI077790	oy35b09.s	788	11	100.0	370	4	BM571767	BM571767	fx05g04.x
c 716	11	100.0	362	1	AI264873	AI264873	qq89b05.x	c 789	11	100.0	370	6	BF675474	BF675474	fx05g04.x
c 717	11	100.0	362	1	AI603027	AI603027	UI-R-AC1-	c 790	11	100.0	370	6	CB588438	CB588438	AGENCOURT
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c 719	11	100.0	362	4	BI712180	BI712180	ie02f03.x	792	11	100.0	370	9	CE808134	CE808134	tigr-g8s-
c 720	11	100.0	362	5	BA877506	BA877506	EX877506	793	11	100.0	371	1	AA847482	AA847482	tiqr-g8s-
c 721	11	100.0	362	5	BY089401	BY089401	BY089401	794	11	100.0	371	1	AA847482	AA847482	tiqr-g8s-
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c 723	11	100.0	362	7	CK983097	CK983097	UMC-bov 0	796	11	100.0	371	1	AI074393	AI074393	tiqr-g8s-
c 724	11	100.0	362	8	AQ509808	AQ509808	HS 2104.A	c 797	11	100.0	371	2	BF836744	BF836744	CM2-HT096
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c 727	11	100.0	363	1	AA106929	AA106929	mm90a06.r	c 800	11	100.0	371	7	CK679457	CK679457	CM2-HT096
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c 729	11	100.0	363	2	BF450967	BF450967	uz75b01.x	c 802	11	100.0	372	1	AU216189	AU216189	UMC-bend
c 730	11	100.0	363	2	AW71715	AW71715	hl70d03.x	c 803	11	100.0	372	2	BF457046	BF457046	UI-M-BX1-
c 731	11	100.0	363	2	BM203714	BM203714	CO258F05-	c 804	11	100.0	372	2	BF709550	BF709550	MI-P-AY0-
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c 735	11	100.0	364	2	BF802542	BF802542	CM0-CI013	c 808	11	100.0	372	8	BI214494	BI214494	AG214494
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c 737	11	100.0	364	2	BB776431	BB776431	BB776431	c 810	11	100.0	372	8	BZ668594	BZ668594	OGDAA60TD
c 738	11	100.0	364	4	BM116392	BM116392	L0835D05-	c 811	11	100.0	372	9	CL421184	CL421184	ZMBBb042
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c 740	11	100.0	364	4	BM226756	BM226756	BM226756	c 813	11	100.0	373	1	AA244580	AA244580	mx07g04.x
c 741	11	100.0	365	1	AI040935	AI040935	ov53a11.x	c 814	11	100.0	373	1	AA598613	AA598613	ae35g01.s
c 742	11	100.0	365	1	AA411993	AA411993	zt68f09.s	c 815	11	100.0	373	4	AG244556	AG244556	602356627
c 743	11	100.0	365	5	BM208377	BM208377	CO62E04-	c 816	11	100.0	373	4	BJ372191	BJ372191	UI-R-CV0-
c 744	11	100.0	365	5	BM101468	BM101468	BM101468	c 817	11	100.0	373	4	BJ251464	BJ251464	UI-R-CV0-
c 745	11	100.0	365	5	BY303072	BY303072	BY303072	c 818	11	100.0	373	6	C44477	C44477	C44477
c 746	11	100.0	365	6	BY675423	BY675423	BY675423	c 819	11	100.0	373	7	CO942010	CO942010	UMC-peov3
c 747	11	100.0	365	6	CB158018	CB158018	K-EST0217	c 820	11	100.0	373	7	Z30205	Z30205	HHEA27G.Atr
c 748	11	100.0	365	7	CK685853	CK685853	ZF101-P00	c 821	11	100.0	373	8	AQ098544	AQ098544	HS_3050.A
c 749	11	100.0	366	1	AI493416	AI493416	tg85h05.x	c 822	11	100.0	374	1	AA895642	AA895642	vx47g08.r
c 750	11	100.0	366	1	AU023287	AU023287	U245b03.x	c 823	11	100.0	374	1	AI085001	AI085001	ow88d01.s
c 751	11	100.0	366	2	BF319884	BF319884	U245b03.x	c 824	11	100.0	374	1	AI168559	AI168559	ow88d01.s
c 752	11	100.0	366	2	BF765234	BF765234	IL2-CS005	c 825	11	100.0	374	2	AW512529	AW512529	tx88e05.x
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833	11	100.0	374	8	BZ831302	CH240.190	BZ831302	CH240.190	C 906	11	100.0	381	8	BZ408823	BZ408823
834	11	100.0	374	9	CG999029	ZNMBB5052	CG999029	ZNMBB5052	C 907	11	100.0	381	8	BZ531666	BZ531666
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836	11	100.0	375	1	AJ803343	AJ803343	AJ803343	AJ803343	C 909	11	100.0	381	9	CG617603	CG617603
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838	11	100.0	375	4	BG220531	RST40317	BG220531	RST40317	C 911	11	100.0	382	1	AI273536	AI273536
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840	11	100.0	375	5	BY424815	BY424815	BY424815	BY424815	C 913	11	100.0	382	2	BB791916	BB791916
841	11	100.0	375	6	C48076	C48076	C48076	C48076	C 914	11	100.0	382	2	BB796774	BB796774
842	11	100.0	375	6	CN860856	000823AAF	CN860856	000823AAF	C 915	11	100.0	382	2	BB836665	BB836665
843	11	100.0	375	8	CC060890	MUGQ_CH25	CC060890	MUGQ_CH25	C 916	11	100.0	382	4	BI432456	BI432456
844	11	100.0	375	9	AG192260	Pan_Crogl	AG192260	Pan_Crogl	C 917	11	100.0	382	5	BY504862	BY504862
845	11	100.0	376	5	BY497583	BY497583	BY497583	BY497583	C 918	11	100.0	382	7	CK755430	CK755430
846	11	100.0	376	6	BY700279	BY700279	BY700279	BY700279	C 919	11	100.0	382	7	CO947194	CO947194
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851	11	100.0	377	1	AI581526	ar92a07.x	AI581526	ar92a07.x	C 924	11	100.0	383	1	AA630656	AA630656
852	11	100.0	377	1	AL700193	DKFZp686L	AL700193	DKFZp686L	C 925	11	100.0	383	2	AW305310	AW305310
853	11	100.0	377	1	AV645626	AV645626	AV645626	AV645626	C 926	11	100.0	383	5	BU953421	BU953421
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861	11	100.0	377	7	CA036680	ssalob007	CA036680	ssalob007	C 934	11	100.0	384	5	BQ478033	BQ478033
862	11	100.0	377	7	CN654272	UNC-bcl.0	CN654272	UNC-bcl.0	C 935	11	100.0	384	5	BQ478033	BQ478033
863	11	100.0	377	7	CN654507	UNC-bend	CN654507	UNC-bend	C 936	11	100.0	384	5	BY422263	BY422263
864	11	100.0	377	9	W05044	za78f11.r1	W05044	za78f11.r1	C 937	11	100.0	384	5	BY441769	BY441769
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870	11	100.0	378	5	BY406738	BY406738	BY406738	BY406738	C 943	11	100.0	385	1	AA583439	AA583439
871	11	100.0	378	6	BY416940	BY416940	BY416940	BY416940	C 944	11	100.0	385	1	BB813451	BB813451
872	11	100.0	378	6	BY528818	BY528818	BY528818	BY528818	C 945	11	100.0	385	2	BE692943	BE692943
873	11	100.0	378	6	BY684420	BY684420	BY684420	BY684420	C 946	11	100.0	385	4	BG877971	BG877971
874	11	100.0	378	6	CB122067	K-EST0169	CB122067	K-EST0169	C 947	11	100.0	385	4	BI466030	BI466030
875	11	100.0	378	6	CB451364	CB451364	CB451364	CB451364	C 948	11	100.0	385	5	BU755653	BU755653
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877	11	100.0	378	8	B69095	CV088744	B69095	CV088744	C 950	11	100.0	385	6	BY659434	BY659434
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879	11	100.0	379	1	AA792995	AA792995	AA792995	AA792995	C 952	11	100.0	385	6	BY701711	BY701711
880	11	100.0	379	1	AI933724	AI933724	AI933724	AI933724	C 953	11	100.0	385	7	CO304289	CO304289
881	11	100.0	379	1	AU023286	AU023286	AU023286	AU023286	C 954	11	100.0	386	1	AA636558	AA636558
882	11	100.0	379	1	AV523891	AV523891	AV523891	AV523891	C 955	11	100.0	386	1	AA675643	AA675643
883	11	100.0	379	1	AV888317	AV888317	AV888317	AV888317	C 956	11	100.0	386	1	AI342284	AI342284
884	11	100.0	379	1	AA398664	AA398664	AA398664	AA398664	C 957	11	100.0	386	1	AI476083	AI476083
885	11	100.0	379	2	BE467712	ve02q05.x	BE467712	ve02q05.x	C 958	11	100.0	386	1	AI826973	AI826973
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888	11	100.0	379	5	BY440948	BY440948	BY440948	BY440948	C 961	11	100.0	386	2	AW008543	AW008543
889	11	100.0	379	8	CO239333	WS00725.B	CO239333	WS00725.B	C 962	11	100.0	386	2	AW664727	AW664727
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892	11	100.0	379	9	CE068356	tigr-g88-	CE068356	tigr-g88-	C 965	11	100.0	386	5	BY442065	BY442065
893	11	100.0	379	9	CL420253	ZMMBB042	CL420253	ZMMBB042	C 966	11	100.0	386	5	BY449302	BY449302
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c 981      11 100.0      387 4 BM313705 ih05c08.x
c 982      11 100.0      387 6 BY644484 BY644484
c 983      11 100.0      387 7 CN917937 030203ABP
c 984      11 100.0      387 7 CN952033 C0504C04
c 985      11 100.0      388 2 BE824747
c 986      11 100.0      388 4 BG583821
c 987      11 100.0      388 5 BM899081
c 988      11 100.0      388 6 BY644485
c 989      11 100.0      388 6 BY672036
c 990      11 100.0      388 6 BY684940
c 991      11 100.0      388 7 C0944620
c 992      11 100.0      388 7 CV351671
c 993      11 100.0      388 7 D54869
c 994      11 100.0      388 8 AQ266797
c 995      11 100.0      388 8 B2408816
c 996      11 100.0      388 9 CG011634
c 997      11 100.0      388 9 CG702278
c 998      11 100.0      388 9 CU260354
c 999      11 100.0      389 1 AA834175
c1000     11 100.0      389 1 AA185175
```

```
AA881812 vx27g02.i
A1049540 an30b12.x
AA099542 zk85g11.s
AJ690317 AJ690317
A180213 zp35f07.s
A062730 A062730
AA598477 ae38e09.s
BM313705 ih05c08.x
BY644484 BY644484
CN917937 030203ABP
CN952033 C0504C04
BE824747 C0504C04
BG583821 EST485578
BM899081 UI-M-D01-
BY644485 BY644485
BY672036 BY672036
BY684940 BY684940
C0944620 UMC-P4mm3
CV351671 MR3-GN002
D54869 HUM156E04B
AQ266797 RPC111-76
B2408816 ZGABM64TC
CG011634 ZUAG210TV
CG702278 ZMVBBC011
CU260354 ZMVBBD061
AA834175 of14f06.s
AA185175 mt95h08.i
```

ALIGNMENTS

```
RESULT 1
AZ636663      43 bp  DNA      linear      GSS 13-DEC-2000
LOCUS      IM0495D12R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION      Clone UUGCLM0495D12 R, genomic survey sequence.
```

```
ACCESSION      AZ636663
VERSION      AZ636663.1
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D. Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
```

```
TITLE      Unpublished (2000)
JOURNAL      Contact: Robert B. Weiss
COMMENT      University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0495 row: D column: 12
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 43.
              Location/Qualifiers
```

```
FEATURES
source
1..43
/mol_type="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0495D12"
/sex="Male"
```

ORIGIN

```
Query Match      100.0%; Score 11; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
        |||||
Db       2 CTTTGGCACTA 12
```

```
RESULT 2
CO866272/c
LOCUS      Mdfirt3046b04.y1 Mdfirt Malus x domestica cDNA clone Mdfirt3046b04 5',
DEFINITION      mRNA sequence.
```

```
ACCESSION      CO866272
VERSION      CO866272.1
KEYWORDS      EST.
SOURCE      Malus x domestica (cultivated apple)
ORGANISM      Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
```

```
REFERENCE
AUTHORS      Korban,S., Vodkin,L., Liu,L., Gasic,K., Gonzales,O., Hernandez,A.,
              Aldwinckle,H., Malnoy,M., Carroll,N., Goldsbrough,P., Orvis,K.,
              Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T.,
              Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Ronko,I.,
              Tsagarisvili,R., Kennedy,S., Waterston,R., and Wilson,R.
              Apple Functional Genomics grant - NSF 0321702
              Unpublished (2004)
```

```
TITLE      Contact: Schuyler S. Korban
JOURNAL      Apple Functional Genomics grant - NSF 0321702
COMMENT      Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              Library materials provided by: Schuyler S. Korban Library
              constructed by: K. Gasic Library sequenced by: Washington
              University Genome Sequencing Center
              WashU EST name: aa152a02.y1
              Seq primer: -40UP from Gibco
              High quality sequence stop: 68.
              Location/Qualifiers
```

```
FEATURES
source
1..68
/mol_type="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="Mdfirt3046b04"
/lab_host="DH10B ampicillin resistant"
```



```

/clone lib="Mdfirt"
/Note="Vector: pBluescript II SK (+); Site 1: NotI;
Site 2: EcoRI; Total RNA was extracted separately from
each stage (young fruitlet (1cm), young fruitlet (1 cm
dia.), young fruitlet (12cm dia.), maturing fruit I,
maturing fruit II, mature fruit), using the 'pine tree'
method. Poly(A)+mRNA was isolated twice from total RNA
from each stage using the Oligotex Direct mRNA kit
(Qiagen). mRNA was reverse transcribed into double
stranded cDNA using a modified oligo18(dT) primer with an
identifying tag sequence (see table below). cDNA's from
different stages were pooled in equal amounts before
adaptor ligation. Tag identification when sequencing from
5' end: Stage 1 (young fruitlet) insert 18(A)TCGTG; Stage
2 (young fruitlet 1cm dia) insert 18(A)TCGTG; Stage 3
(young fruitlet 12cm dia) insert 18(A)TCGTG; Stage 4
(maturing fruit I) insert 18(A)TCGA; Stage 5 (maturing
fruit II) insert 18(A)TCGA; Stage 6 (mature fruit) insert
18(A)TCGTG; Tag identification when sequencing from 3'
end: Stage 1 (young fruitlet) CACGA18(T) insert; Stage 2
(young fruitlet 1cm dia) CACGA18(T) insert; Stage 3 (young
fruitlet 12cm dia) ACCGA18(T) insert; Stage 4 (maturing
fruit I) TCGA18(T) insert; Stage 5 (maturing fruit II)
TCGA18(T) insert; Stage 6 (mature fruit) ACCGA18(T)
insert. Double stranded cDNAs were size selected (more
than 450 bp), adaptor with EcoRI adapters at both ends
and then digested with NotI. The cDNAs were then
directionally cloned into EcoRI-NotI digested pBS II SK(+)
phagemid vector(Stratagene). Identification of adaptors
and tags in 5'-end sequenced clones:
<Vector>...TAAGCTT<End Vector><Start
EcoRI adaptor>GATTCGAATTCATGTGTGGG <End
EcoRI adaptor><Start Insert>...AAAAAAAAAAAAAAAA<End
Insert> <Start Tag>TCGA<End Tag><Start
NotI site>/Vector>GGGCCCGCCGCGG... The total number of
white colony forming units (cfu) in the primary library
before amplification was 2.1x10^6 cfu (colony forming
units). The background of empty clones was less than 1%.
Inserts ranged from 0.5kb to 4 kb, as determined by PCR.
Purified plasmid DNA from the primary library was
converted to single-stranded circles and used as a
template for PCR amplification using the T7 and T3 priming
sites flanking the cloned cDNA inserts. The purified PCR
products, representing the entire cloned cDNA population,
were used as a driver for normalization. Hybridization
between the single-stranded library and the PCR products
was carried out for 4 hours at 30C. Unhybridized
single-stranded DNA circles were separated from hybridized
DNA rendered partially double-stranded and electroporated
into DH10B cells to generate the normalized library. The
total number of clones with insert was 5.6x10^6 cfu.
Background of empty clones was less than 1%."

```

## ORIGIN

```

Query Match      100.0%; Score 11; DB 7; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
DB      34 CTTTGGCACTA 24

```

## RESULT 3

```

T77835
LOCUS      yd16c08.s1 Soares fetal liver spleen INF1LS Homo sapiens cDNA clone
DEFINITION IMAGE:108398 3', mRNA sequence.
ACCESSION T77835
VERSION    T77835.1 GI:695038
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

```

```

REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 72)
              Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
              Holman,M., Hultkin,L., Kucaba,T., Le,M., Lennon,G., Marra,M.,
              Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
              Trivasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
              Wilson,R.
              The WashU-Merck EST Project
              Unpublished (1995)
              Contact: Wilson RK
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              Insert Size: 222
              Contact: Wilson RK
              JOURNAL
              COMMENT      Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              Insert Size: 222
              Source: IMAGE Consortium, LLNL This clone is available royalty-free
              through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
              for further information.
              Insert Length: 222 Std Error: 0.00
              Seq primer: -21ml3
              High quality sequence stop: 255.
              Location/Qualifiers
                1..72
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="GDB:464015"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:108398"
                  /sex="male"
                  /dev_stage="20 week-post conception fetus"
                  /lab_host="DH10B (ampicillin resistant)"
                  /clone_lib="Soares fetal liver spleen INF1LS"
                  /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
                  with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                  1st strand cDNA was primed with a Pac I - oligo(dT) primer
                  [5' AACTGGAAGAAATTAATAAGATCTTTTCTTTTCTTTT 3',
                  double-stranded cDNA was ligated to Eco RI adaptors
                  (Pharmacia), digested with Pac I and cloned into the Pac I
                  and Eco RI sites of the modified pT73 vector. Library
                  went through one round of normalization. Library
                  constructed by Bento Soares and M.Fatima Bonaldo."

```

## FEATURES

```

source
  1..72
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="GDB:464015"
    /db_xref="taxon:9606"
    /clone="IMAGE:108398"
    /sex="male"
    /dev_stage="20 week-post conception fetus"
    /lab_host="DH10B (ampicillin resistant)"
    /clone_lib="Soares fetal liver spleen INF1LS"
    /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
    with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
    1st strand cDNA was primed with a Pac I - oligo(dT) primer
    [5' AACTGGAAGAAATTAATAAGATCTTTTCTTTTCTTTT 3',
    double-stranded cDNA was ligated to Eco RI adaptors
    (Pharmacia), digested with Pac I and cloned into the Pac I
    and Eco RI sites of the modified pT73 vector. Library
    went through one round of normalization. Library
    constructed by Bento Soares and M.Fatima Bonaldo."

```

## ORIGIN

```

Query Match      100.0%; Score 11; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
DB      17 CTTTGGCACTA 27

```

## RESULT 4

```

CG668957
LOCUS      OST465420 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST465420,
DEFINITION mRNA sequence.
ACCESSION CG668957
VERSION    CG668957.1 GI:37492806
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

## REFERENCE

```

AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 87)
              Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
              Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
              Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
              Key,B.W., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
              Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
              Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,

```

**TITLE** Zhu, Q., Person, C. and Sands, A.T.  
**JOURNAL** Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
**COMMENT** screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 Contact: Zambrowicz BP  
 OmniBank

Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
**Class:** Gene Trap.

**FEATURES**

source

1. 87  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129Sv/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST465420"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

**ORIGIN**

**Query Match** 100.0%; Score 11; DB 9; Length 87;  
**Best Local Similarity** 100.0%; Pred. No. 1.7e+04;  
**Matches** 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CTTTGGCACTA 11  
 |||||  
**Db** 51 CTTTGGCACTA 61

**RESULT 5**  
**A1631958/c**

**LOCUS** A1631958 88 bp mRNA linear EST 26-APR-1999  
**DEFINITION** wa38b09.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2300345 3'  
 similar to gb:M98326 VALYL-TRNA SYNTHETASE (HUMAN);, mRNA sequence.

**ACCESSION** A1631958  
**VERSION** A1631958.1 GI:4683288  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 88)

**REFERENCE** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

**AUTHORS** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

**JOURNAL** Unpublished (1997)

**COMMENT** Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

**FEATURES**

source

1. 88  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2300345"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Kid11"  
 /note="Organ: kidney; Vector: p7T3D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;

**ORIGIN**

**Query Match** 100.0%; Score 11; DB 1; Length 88;  
**Best Local Similarity** 100.0%; Pred. No. 1.7e+04;  
**Matches** 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CTTTGGCACTA 11  
 |||||  
**Db** 17 CTTTGGCACTA 7

**RESULT 6**

BZ662266/c

**LOCUS** BZ662266 88 bp DNA linear GSS 31-JAN-2003  
**DEFINITION** SALK\_025751.28.05.x Arabidopsis thaliana TDNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_025751.28.05.x, genomic  
 survey sequence.

**ACCESSION** BZ662266  
**VERSION** BZ662266.1 GI:28176379

**KEYWORDS** GSS.

**SOURCE** Arabidopsis thaliana (thale cress)

**ORGANISM** Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 88)

**REFERENCE** Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 Shinn, P., Zimmermann, J. and Ecker, J.R.

**AUTHORS** A Sequence-Indexed Library of Insertion Mutations in the

**TITLE** Arabidopsis Genome

**JOURNAL** Unpublished (2001)

**COMMENT** Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

**Class:** TDNA tagged.

**FEATURES** Location/Qualifiers

source

1. 88

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="SALK\_025751.28.05.x"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

**ORIGIN**

**Query Match** 100.0%; Score 11; DB 8; Length 88;  
**Best Local Similarity** 100.0%; Pred. No. 1.7e+04;  
**Matches** 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CTTTGGCACTA 11  
 |||||  
**Db** 68 CTTTGGCACTA 58

Plasmid DNA from the normalized library NCI CGAP Kid3 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (Clones 132376-132391, 1456007-1456775, and  
 1500552-1502855). Subtraction by Bento Soares and M.  
 Fatima Bonaldo.

```

RESULT 7
BG409256
LOCUS
DEFINITION
  91 bp mRNA linear EST 13-MAR-2001
  9b89g12.y1 Moss EST library PPG Physcomitrella patens cDNA clone
  PEP_SOURCE_ID:PPG_CopyA-121423 5', mRNA sequence.
ACCESSION
  BG409256
VERSION
  BG409256.1 GI:13315601
KEYWORDS
  EST.
SOURCE
  Physcomitrella patens
  Physcomitrella patens
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
  Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE
  1 (bases 1 to 91)
  Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C.,
  Clifton, S., Marra, M., Hillier, B., Pape, D., Martin, J., Wyllie, T.,
  Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
  Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
  Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
  Leeds/Wash U Moss EST Project
  Unpublished (1999)
  Contact: Ralph Quatrano
  Leeds/Wash U Moss EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: estwatson.wustl.edu
  Libraries were constructed by Dr. Stavros Bashardes as part of the
  Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
  Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
  University Genome Sequencing Center For information on obtaining a
  clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
  Putative full length read
  vector to vector length is 92
  Seq primer: -40RP from Gibco.
  Location/Qualifiers
    1..91
      /organism="Physcomitrella patens"
      /mol_type="mRNA"
      /db_xref="taxon:3218"
      /clone="PEP_SOURCE_ID:PPG_CopyA-121423"
      /tissue_type="gametophore: 30 day old tissue,
      ammonium-grown"
      /lab_host="DH10B"
      /clone_lib="Moss EST library PPG"
      /note="Vector: pAMP1; Construction of the cDNA library was
      performed by Dr. W. Gregg Clark using a modification of
      the cDNA synthesis protocol developed in the laboratory of
      Dr. Michael Lovett by Dr. Yulia Korshunova (personal
      communication). First polyA + RNA was isolated from total
      gametophore RNA using oligo dT magnetic beads. Following
      this, first strand cDNA synthesis was performed on the
      bead-bound polyA + RNA, during which an oligonucleotide
      anchor sequence was incorporated onto the 5'-ends of the
      cDNA. PCR amplification was then used to synthesize the
      second strand, to amplify the double stranded DNA, and to
      incorporate dUTP containing sequences into the ends of the
      double stranded cDNA. This DNA was size selected and
      cloned into pAMP1 using the CloneAMP pAMP1 System (Life
      Technologies, GibcoBRL) for cloning amplification products
      by a non-restriction site dependant process. The cloning
      was directional based on sequence asymmetry introduced at
      the ends during PCR amplification. The 3' cDNA ends are
      proximal to the NotI site of the multiple cloning site in
      pAMP1. This annealing mixture was transformed into
      chemically competent DH10B cells and selected for
      ampicillin resistant growth. The resulting clones (about
      330,000) were pooled to make the library."
FEATURES
  source
    1..91
      /organism="Physcomitrella patens"
      /mol_type="mRNA"
      /db_xref="taxon:3218"
      /clone="PEP_SOURCE_ID:PPG_CopyA-121423"
      /tissue_type="gametophore: 30 day old tissue,
      ammonium-grown"
      /lab_host="DH10B"
      /clone_lib="Moss EST library PPG"
      /note="Vector: pAMP1; Construction of the cDNA library was
      performed by Dr. W. Gregg Clark using a modification of
      the cDNA synthesis protocol developed in the laboratory of
      Dr. Michael Lovett by Dr. Yulia Korshunova (personal
      communication). First polyA + RNA was isolated from total
      gametophore RNA using oligo dT magnetic beads. Following
      this, first strand cDNA synthesis was performed on the
      bead-bound polyA + RNA, during which an oligonucleotide
      anchor sequence was incorporated onto the 5'-ends of the
      cDNA. PCR amplification was then used to synthesize the
      second strand, to amplify the double stranded DNA, and to
      incorporate dUTP containing sequences into the ends of the
      double stranded cDNA. This DNA was size selected and
      cloned into pAMP1 using the CloneAMP pAMP1 System (Life
      Technologies, GibcoBRL) for cloning amplification products
      by a non-restriction site dependant process. The cloning
      was directional based on sequence asymmetry introduced at
      the ends during PCR amplification. The 3' cDNA ends are
      proximal to the NotI site of the multiple cloning site in
      pAMP1. This annealing mixture was transformed into
      chemically competent DH10B cells and selected for
      ampicillin resistant growth. The resulting clones (about
      330,000) were pooled to make the library."
ORIGIN
  Query Match
  Best Local Similarity 100.0%; Score 11; DB 4; Length 91;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  RESULT 8
  BG409256
  LOCUS
  DEFINITION
    106 bp mRNA linear EST 21-JUN-2000
    QV1-HT0474-070300-098-g07 HT0474 Homo sapiens cDNA, mRNA sequence.
  ACCESSION
    BE165421
  VERSION
    BE165421.1 GI:8628142
  KEYWORDS
    EST.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 106)
    Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
    Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
    Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
    Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
    O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
    Simpson, A.J.
    Shotgun sequencing of the human transcriptome with ORF expressed
    sequence tags
    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  JOURNAL
    MEDLINE
    PUBMED
    10737800
  COMMENT
    Contact: Simpson A.J.G.
    Laboratory of Cancer Genetics
    Ludwig Institute for Cancer Research
    Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
    Brazil
    Tel: +55-11-2704922
    Fax: +55-11-2707001
    Email: asimpson@ludwig.org.br
    This sequence was derived from the FAPESP/LICR Human Cancer Genome
    Project. This entry can be seen in the following URL
    (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=4t2=QV1-HT0474-070
    300-098-g07&t3=2000-03-07&t4=1)
    Seq primer: puc 18 forward
    High quality sequence start: 9
    High quality sequence stop: 106.
    Location/Qualifiers
      1..106
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /dev_stage="Adult"
        /clone_lib="HT0474"
        /note="Organ: head neck; Vector: puc18; Site_1: SmaI;
        Site_2: SmaI; A mini-library was made by cloning products
        derived from ORESTES PCR (U.S. Letters Patent application
        No. 196,716 - Ludwig Institute for Cancer Research)
        profiles into the pUC 18 vector. Reverse transcription of
        tissue mRNA and cDNA amplification were performed under
        low stringency conditions."
  ORIGIN
    Query Match
    Best Local Similarity 100.0%; Score 11; DB 2; Length 106;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    1 CTTTGGCACTA 11
    |||||
    7 CTTTGGCACTA 17
    |||||

  RESULT 9
  CF776000/c
  LOCUS
  DEFINITION
    100.0%; Pred. No. 1.7e+04;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    1 CTTTGGCACTA 11
    |||||
    24 CTTTGGCACTA 34
    |||||

  ORIGIN
    Query Match
    Best Local Similarity 100.0%; Score 11; DB 4; Length 91;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    1 CTTTGGCACTA 11
    |||||
    24 CTTTGGCACTA 34
    |||||

```

LOCUS CF776000 107 bp mRNA linear EST 20-OCT-2003  
DEFINITION jaa28e10.y1 Anolis sagrei limb bud 2 Anolis sagrei cDNA 5' similar  
to TR:O95630 O95630 AMSH. ;, mRNA sequence.  
ACCESSION CF776000  
VERSION CF776000  
KEYWORDS EST.  
SOURCE CF776000.1 GI:37762717  
ORGANISM Anolis sagrei (brown anole)  
REFERENCE Anolis sagrei  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.  
1 (bases 1 to 107)  
Loeser, J., Gibson-Brown, J., Sanger, T.J., Langwith, S., Murphy, C.,  
Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylie, T.,  
Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E.,  
Bennett, J., Ronko, I., Tsagareishvili, R., Maguire, L., Kennedy, S.,  
Waterston, R. and Wilson, R.  
Packard/Washington University Lizard Limb Bud EST Project  
Unpublished (2003)  
Contact: Jeremy Gibson-Brown  
Packard/Washington University Lizard Limb Bud EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library was constructed by Jeremy Gibson-Brown DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Jeremy Gibson-Brown  
(gibbro@biology.wustl.edu)  
Seq primer: T7.  
FEATURES Location/Qualifiers  
source 1..107  
/organism="Anolis sagrei"  
/mol\_type="mRNA"  
/db\_xref="taxon:38937"  
/lab\_host="DH10B"  
/clone\_lib="Anolis sagrei limb bud 2"  
/note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:  
BamHI; 1st strand primed with an oligo (dT) primer; double  
stranded cDNA was cloned into the EcoRI and BamHI sites of  
the pBluescript SK+ vector. Primary library;  
non-amplified."  
ORIGIN  
Query Match 100.0%; Score 11; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTGGCACTA 11  
|||||  
DB 26 CTTTGGCACTA 16  
RESULT 10  
AZ517183/c 113 bp DNA linear GSS 16-OCT-2000  
LOCUS RPCI-11-5P24.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-5P24,  
genomic survey sequence.  
DEFINITION  
ACCESSION AZ517183  
VERSION AZ517183.1 GI:10826158  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 113)  
AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and  
Venter, J.C.  
TITLE BAC end sequences of library RPCI-11  
JOURNAL Unpublished (1997)  
COMMENT Other\_GSSs: RPCI11-5P24.TVB  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics

The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhac@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
Research Genet cs (info@resgen.com). BAC end search page:  
http://www.tigr.org/cdb/humgen/bac\_end\_search/bac\_end\_search.html.  
This BAC end was generated during the R&D process and may have  
higher chance of clone tracking errors.  
Seq primer: SP6  
Class: BAC ends  
FEATURES Location/Qualifiers  
source 1..113  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="GDB:7501919"  
/db\_xref="taxon:9606"  
/clone="RPCI-11-5P24"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/clone\_lib="RPCI-11"  
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
RPCI11 Human Male BAC Library"  
ORIGIN  
Query Match 100.0%; Score 11; DB 8; Length 113;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTGGCACTA 11  
|||||  
DB 94 CTTTGGCACTA 84  
RESULT 11  
B1130927 116 bp mRNA linear EST 31-DEC-2001  
LOCUS G112P81Y Populus cambium cDNA library Populus tremula x Populus  
tremuloides cDNA, mRNA sequence.  
DEFINITION  
ACCESSION B1130927  
VERSION B1130927.1 GI:18014898  
KEYWORDS EST.  
SOURCE Populus tremula x Populus tremuloides  
ORGANISM Populus tremula x Populus tremuloides  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.  
REFERENCE 1 (bases 1 to 116)  
AUTHORS Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H.,  
Hiltunen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlnerao, R.,  
Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M.,  
Sandberg, G. and Lundberg, J.  
Gene expression in Populus  
Contact: Erlandsson R  
Department of Biotechnology  
Royal Institute of Technology  
Teknikringen 30, Stockholm S-10044, Sweden  
Tel: 46 8 790 8287  
Fax: 46 8 245452  
Email: riker@biochem.kth.se.  
Location/Qualifiers  
source 1..116  
/organism="Populus tremula x Populus tremuloides"  
/mol\_type="mRNA"  
/db\_xref="taxon:47664"  
/clone\_lib="Populus cambium cDNA library"  
/note="Organ: cambium"  
ORIGIN

Query Match 100.0%; Score 11; DB 4; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
 |||||  
 Db 32 CTTTGGCACTA 42

RESULT 12  
 BF901301/c  
 LOCUS  
 DEFINITION IL2-MT0179-081200-288-B12\_1 MT0179 Homo sapiens cDNA, mRNA  
 sequence.  
 ACCESSION BF901301  
 VERSION BF901301.1 GI:12292760  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 120)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=IL2&t2=IL2-MT0179-  
 081200-288-B12.1&t3=2000-12-08&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 116.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="MT0179"  
 /note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the puc 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."

ORIGIN  
 Query Match 100.0%; Score 11; DB 2; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTGGCACTA 11  
 |||||  
 Db 19 CTTTGGCACTA 9

FEATURES  
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 1..120  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="MT0179"  
 /note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the puc 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."

ORIGIN  
 Query Match 100.0%; Score 11; DB 2; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTGGCACTA 11  
 |||||  
 Db 19 CTTTGGCACTA 9

RESULT 13  
 AW551508  
 LOCUS  
 DEFINITION L0079H06-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA  
 Library Mus musculus cDNA clone L0079H06 3', mRNA sequence.

ACCESSION AW551508  
 VERSION AW551508.2 GI:31566650  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)

ORGANISM  
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 120)  
 AUTHORS Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,  
 Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagatani,R., Doi,H.,  
 Wood,W.H. III, Becker,K.G. and Ko,M.S.H.

TITLE Genome-wide expression profiling of mid-gestation placenta and  
 embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

MEDLINE 20381348  
 PUBMED 10922068

COMMENT On Mar 7, 2000 this sequence version replaced gi:7196936.  
 Contact: George J. Kargul  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@gsun.grc.nia.nih.gov

Plate: L0079 row: H column: 06  
 Seq primer: -21M13 Forward  
 High quality sequence stop: 120  
 POLYA=Yes.

Location/Qualifiers  
 1..120  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="niaEST:L0079H06-3"  
 /db\_xref="taxon:10090"  
 /clone="L0079H06"  
 /sex="female"  
 /dev\_stage="12.5dpc"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse E12.5 Female Mesonephros and Gonads  
 cDNA Library"

/note="Vector: pSPORT1 (Gibco/BRL Life Technology);  
 Site 1: SalI; Site 2: NotI; Total RNAs were extracted from  
 2 Mesonephros. The double-stranded cDNA was synthesized  
 by Gibco's kit with an Oligo(dT) primer [NotI  
 primer-adaptor from GibcoBRL]  
 [5'-PGACTAGTCTAGATCGAGCGCGCCCTTTT-3'] from  
 3.42ug of total RNA. The double-stranded cDNAs were  
 treated with T4 DNA polymerase and purified by  
 ethanol-precipitation. The cDNAs were ligated to  
 lone-linker L1-Sal3 (include SalI sequence). The cDNAs  
 were purified by phenol/chloroform and separated from  
 free linkers by Centricon 100. Then, cDNAs were amplified  
 by long-range high fidelity PCR using Takara's Ex Taq  
 polymerase. Then, the cDNAs were purified by  
 phenol/chloroform and by Centricon 100. The cDNAs were  
 digested with SalI and NotI enzymes. Then, the cDNAs were  
 size selected by Gibco's Size Fractionation Column. The  
 cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid  
 vector. The DH10B E. coli host was transformed with the  
 ligation mixture by chemical method. The library was  
 constructed by Xiaohong Wang."

ORIGIN  
 Query Match 100.0%; Score 11; DB 2; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTGGCACTA 11  
 |||||

```

Db          45 CTTTGGCACTA 55

RESULT 14
LOCUS      CK105615
DEFINITION UA25DPA07.5Pr Populus dormant cambium cDNA library Populus tremula
            cDNA clone UA25DPA07 5', mRNA sequence.
ACCESSION  CK105615
VERSION     CK105615.1 GI:38589940
KEYWORDS   EST.
SOURCE     Populus tremula
ORGANISM   Populus tremula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE  1 (bases 1 to 120)
AUTHORS    Sterky,F., Bhalarao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,
            Brunner,A.M., Campaa,L., Jonsson-Lindvall,J., Tandre,K.,
            Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalarao,R.P.,
            Nilsson,O., Sandberg,G., Karlsson,J., Lundberg,J. and Jansson,S.
            A Populus EST resource for functional genomics
            Other ESTs: UA25DPA07
            Unpublished (2003)
TITLE      Contact: Bo Segerman
JOURNAL    Umea Plant Science Center, Department of Plant Physiology
COMMENT    Umea University
            901 87 Umea, Sweden
            Tel: +46 90 786 5279
            Fax: +46 90 786 6676
            Email: bo.segerman@plantphys.umu.se.

FEATURES   source
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            /organism="Populus tremula"
            /mol_type="mRNA"
            /db_xref="taxon:113636"
            /clone="UA25DPA07"
            /tissue_type="Dormant cambium"
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ORIGIN
Query Match      100.0%; Score 11; DB 7; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
        |||||
        58 CTTTGGCACTA 68

Db          45 CTTTGGCACTA 55

RESULT 15
LOCUS      BF352764
DEFINITION IL3-HT0619-050700-199-D07 HT0619 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF352764
VERSION     BF352764.1 GI:11311838
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 121)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
TITLE      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL    2002663
MEDLINE    10737800
PUBMED

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-HT0619-
050700-199-D07&t3=2000-07-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 121.
Location/Qualifiers
1..121
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0619"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 11; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
        |||||
        18 CTTTGGCACTA 28

RESULT 16
LOCUS      A2759838
DEFINITION 1M0552P23R Mouse 10kb plasmid UUGCM library Mus musculus genomic
            clone UUGCM0552P23 R, genomic survey sequence.
ACCESSION  A2759838
VERSION     A2759838.1 GI:12867034
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 122)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
TITLE      Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112 USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0852 row: P column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 122.

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FEATURES  
source

Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0552P23"  
/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMP42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL1, the vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 100.0%; Score 11; DB 8; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 14 CTTTGGCACTA 24

## RESULT 17

CA345114/c  
LOCUS 127 bp mRNA linear EST 05-NOV-2002  
DEFINITION 675650 NCCOWA 1RT Oncorhynchus mykiss cDNA clone 1RT85B06\_D\_A03 5', mRNA sequence.  
ACCESSION CA345114  
VERSION CA345114.1 GI:24590285  
KEYWORDS EST.  
SOURCE Oncorhynchus mykiss (rainbow trout)  
ORGANISM Oncorhynchus mykiss  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

## REFERENCE

AUTHORS Koop, B., Gahr, S.A., Palti, Y., and Quackenbush, J.  
TITLE Sequence analysis of a rainbow trout cDNA library and creation of a gene index  
JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)  
COMMENT Contact: Rexroad CE  
USDA, ARS, National Center for Cool and Cold Water Aquaculture  
11876 Leetown Road, Kearneysville, WV 25430, USA  
Tel: 304 724 8340 x2129  
Fax: 304 725 0351

Email: crexroad@nccowa.ars.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified by cross match v0.990329.

Seq primer: ACGGATACAAATTCACACAGGA.

## FEATURES

## source

1. .127  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"

FEATURES  
source

/db\_xref="taxon:8022"  
/clone="1RT85B06\_D\_A03"  
/tissue type="pooled"  
/lab host="DH10B"  
/clone lib="NCCOWA 1RT"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."

## ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 39 CTTTGGCACTA 29

## RESULT 18

CB352552/c  
LOCUS 129 bp mRNA linear EST 10-NOV-2003  
DEFINITION ZF001-P00003-DPB-F2-D\_H03 GISZF001 Danio rerio cDNA clone IMAGE:6892759 5', similar to fd56h03.y1 Zebrafish Washu PIMG EST  
Danio rerio cDNA clone IMAGE:373781 5', similar to SWACDM\_RAI  
P08503 ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR, mRNA sequence.

ACCESSION CB352552

VERSION CB352552.1 GI:28989293

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

## ORGANISM

Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS Mathavan, S., Wei, C., Thoreau, H., Chia, J.M. and Ruan, Y.

TITLE Genome Institute of Singapore, Zebrafish EST Collection

JOURNAL Unpublished (2003)

COMMENT Contact: Ruan Y

Cloning and Sequencing

Genome Institute of Singapore

60 Biopolis Street, #02-01, Genome, Singapore 138672

Tel: +65 6478 8073

Fax: +65 6478 9059

Email: ruanyj@gis.a-star.edu.sg

GIS Clone ID: ZF001-P00003-PP\_P06

PCR Primers

FORWARD: M13

BACKWARD: M13

Plate: ZF001-P00003-DPB-F2-D

Seq primer: CCGCATACCTGTATAGCA

High quality sequence stop: 129.

## FEATURES

## source

1. .129  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:6892759"  
/tissue type="Embryo"  
/dev stages="7 Different embryonic stages ( From just fertilized Embryos to 72 hours just hatched baby fish )"  
/lab host="DH10B"  
/clone lib="GISZF001"  
/note="Vector: pDNR-LIB; Site 1: Sfi A (GGCATTAGGCC); Site 2: Sfi B (GGCGGCTGGCC); Priming method: Sfi-(drr)30  
Primed; Priming sequence: 5'ATTCTAGA GGCGAGCGGCC  
GACATG(T)30VN; Directionally cloned, 5' cloning site:  
Sfi A site GGCATTAGGCC; 5' linker/adaptor sequence:  
5'AGCAGTGTATCAACGACAGTGGCC; 3' cloning site: Sfi B  
site GGCGGCTGGCC; 3' linker/adaptor sequence: same  
as the priming sequence; Average insert size: 2kb; For  
PCR insert analysis: Use M13 Forward and reverse primers;



Library Amplified Recombinants (inserts): 98; Library complexity: 5x10<sup>6</sup>; Full-length construction (method): SMART, a Clontech method; Library constructed by: S. Mathavan, Chia-Lin Wei, and Yijun Ruan Genome Institute of Singapore"

## ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 95 CTTTGGCACTA 85

## RESULT 19

CG918048/c  
LOCUS CG918048 130 bp DNA linear GSS 12-DEC-2003  
DEFINITION CH240\_137A21.TJ CHORI-240 Bos taurus genomic clone CH240\_137A21,  
genomic survey sequence.

ACCESSION CG918048

VERSION CG918048.1 GI:39777731

KEYWORDS GSS.

SOURCE Bos taurus (cow)

## ORGANISM

Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (bases 1 to 130)

AUTHORS Costa J.N., Mota M. and Caetano A.R.

TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library

CHORI-240

JOURNAL Unpublished (2003)

## COMMENT

Other GSSs: CH240\_137A21.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologicas, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acatano@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm).

Bases shown have Phred quality value equal to or higher than 20.

Bases with quality value below 20 were masked with 'N'.

For BAC library availability, please contact Pieter de Jong

(pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering\_information.htm).

This work was undertaken as part of the International Bovine BAC

Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e

Biotecnologia with financing from Conselho Nacional de

Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil

Plate: 137 row: A column: 21

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 130.

## FEATURES

## source

Location/Qualifiers

1..130

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="breed: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_137A21"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MhoI;

Hereford bull LI Domino 99375; CHORI-240 Bovine BAC

library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 100.0%; Score 11; DB 9; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 113 CTTTGGCACTA 103

## RESULT 20

AA508728/c  
LOCUS AA508728 138 bp mRNA linear EST 18-AUG-1997  
DEFINITION nh88d08.sl NCI\_CGAP\_P8 Homo sapiens cDNA clone IMAGE:957519, mRNA  
sequence.

ACCESSION AA508728

VERSION AA508728.1 GI:2246231

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 138)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuvaqu,

M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CNA Library Preparation: David B. Krizman, Ph.D.

CNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 346 Std Error: 0.00

Seq primer: -40ml3 fwd: ET from Amersham.

## FEATURES

## source

Location/Qualifiers

1..138

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:957519"

/sex="male"

/tissue\_type="prostate"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_P8"

/note="Vector: PAMP10; mRNA made from invasive prostate

tumor, cDNA made by oligo-dT priming. Non-directionally

cloned. Size-selected on agarose gel, average insert

size 600 bp."

## ORIGIN

Query Match 100.0%; Score 11; DB 1; Length 138;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 18 CTTTGGCACTA 8

## RESULT 21

BF545856  
LOCUS BF545856 138 bp mRNA linear EST 11-DEC-2000  
DEFINITION UI-R-BT0-qe-c-01-0-UI.r1 UI-R-BT0 Rattus norvegicus cDNA clone  
BF545856  
BF545856  
BF545856.1 GI:11636963

ACCESSION BF545856

VERSION BF545856.1

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)



```

ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 138)
AUTHORS        Bonaldo,M.F., Lemon,G. and Soares,M.B.
TITLE          Normalization and subtraction: two approaches to facilitate gene
MEDLINE        97044477
PUBMED         889548
COMMENT        Contact: Soares, MB
                Coordinated Laboratory for Computational Genomics
                University of Iowa
                375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
                Tel: 319 335 8250
                Fax: 319 335 9565
                Email: bento-soares@iowa.edu
                cDNA Library Preparation: M.B. Soares Lab Clone distribution:
                clones will be available through Research Genetics (www.regen.com)
                This clone is also available through the I.M.A.G.E. Consortium at
                LLNL (info@image.llnl.gov). IMAGE ID= 1788637
                Seq primer: M13 Forward.
FEATURES       Location/Qualifiers
                1..138
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /strain="Sprague-Dawley"
                /db_xref="taxon:10116"
                /clone="UI-R-B70-qe-c-01-0-UI"
                /dev_stage="adult"
                /lab_host="DH10B (Life Technologies)"
                /clone_lib="UI-R-B70"
                /note="Vector: pTT3D-Pac (Pharmacia) with a modified
                polylinker; Site 1: Not I; Site 2: Eco RI; This library
                (UI-R-B70) consists of a mixture of individually tagged
                normalized libraries constructed from rat hippocampus,
                thalamus, mid-brain, medulla, corpus striatum, cerebral
                cortex and testis. The tag used to identify the source
                tissue is a string of 3-6 nucleotides present between the
                Not I site and the oligo-dT track which allows
                identification of the library of origin of a clone within
                the mixture. This library was then subtracted using a
                driver consisting of a mixture of all clones from UI-R-A0,
                UI-R-A1, UI-R-E0, UI-R-E1, UI-R-E1, UI-R-C0, UI-R-C1, UI-R-C2 and
                UI-R-C2p."
ORIGIN
Query Match      100.0%; Score 11; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
        |||||
DB      127 CTTTGGCACTA 137

RESULT 22
BH055493/c
LOCUS      BH055493      140 bp      DNA      linear      GSS 18-JUL-2001
DEFINITION      RPCI-24-278115.TJ RPCI-24 Mus musculus genomic clone
ACCESSION      BH055493
VERSION        BH055493.1 GI:14862399
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 140)
AUTHORS        Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
                Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
                Russell,D., de Jong,P. and Fraser,C.M.

TITLE          Mouse BAC End Sequences from Library RPCI-24
JOURNAL        Unpublished (1999)
COMMENT        Other GSSs: RPCI-24-278115.TV
                Contact: Shaying Zhao
                Department of Eukaryotic Genomics
                The Institute for Genomic Research
                9712 Medical Center Dr., Rockville, MD 20850, USA
                Tel: 301 838 0200
                Fax: 301 838 0208
                Email: szhao@tigr.org
                Clones are derived from the mouse BAC library RPCI-24. For BAC
                library availability, please contact Pieter de Jong
                (pdejong@mail.cho.org). Clones may be purchased from BACPAC
                Resources (http://www.tigr.org/bacpac/orderingframe.htm). BAC end
                plate: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                Plate: 278 row: I column: 15
                Seq primer: SP6
                Class: BAC ends.
FEATURES       Location/Qualifiers
                1..140
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="RPCI-24-278115"
                /sex="Male"
                /cell_type="Spleen/Brain"
                /clone_lib="RPCI-24"
                /note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
                RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                library was cloned in the pTARBAC1 cloning vector at the
                BamHI sites using MboI partially digested male C57BL/6J
                DNA."
ORIGIN
Query Match      100.0%; Score 11; DB 8; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
        |||||
DB      93 CTTTGGCACTA 83

RESULT 23
AI965679/c
LOCUS      AI965679      141 bp      mRNA      linear      EST 12-JUL-2004
DEFINITION      sc76h06.y1 Gm-cl018 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
                Gm-cl018-852 5', mRNA sequence.
ACCESSION      AI965679
VERSION        AI965679.1 GI:5760388
KEYWORDS        EST.
SOURCE          Glycine max (soybean)
ORGANISM        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                Glycine.
REFERENCE      1 (bases 1 to 141)
AUTHORS        Shoemaker,R., Keim,P., Vodka,L., Erpelding,J., Coryell,V.,
                Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
                Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
                Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
                Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
                McCann,R., Waterston,R. and Wilson,R.
                Public Soybean EST Project
                Unpublished (1999)
                Contact: Shoemaker R/Public Soybean EST Project
                Public Soybean EST Project
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                Tel: 314 286 1800
                Fax: 314 286 1810

```

Email: est@watson.wustl.edu  
 When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 Insert length: 821 Std Error: 0.00  
 High quality sequence stop: 119.

#### FEATURES

Location/Qualifiers  
 1..141  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Williams 82"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl018-852"  
 /tissue\_type="leaves of greenhouse grown plants"  
 /dev\_stage="2-3 weeks old"  
 /lab\_host="DH10B (Gibco BRL)"  
 /clone\_lib="Gm-cl018"  
 /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Expelding."

#### ORIGIN

Query Match 100.0%; Score 11; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 120 CTTTGGCACTA 110

#### RESULT 24

AA717598/6  
 LOCUS  
 DEFINITION  
 vp94a07.r1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1092372 5' similar to gb:M12866 Mouse skeletal muscle actin mRNA, complete cds (MOUSE); mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AA717598.1 GI:2729872  
 EST.  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 146)  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE  
 JOURNAL  
 COMMENT

The WashU-HMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:598604

Trace considered overall poor quality  
 Seq primer: -28ml3 revl ET from Amersham  
 High quality sequence stop: 1.

#### FEATURES

Location/Qualifiers  
 1..146  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1092372"  
 /tissue\_type="diaphragm"  
 /dev\_stage="adult"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stratagene mouse diaphragm (#937303)"  
 /note="Organ: diaphragm; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTITTTTTTTT 3"

#### ORIGIN

Query Match 100.0%; Score 11; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 109 CTTTGGCACTA 99

#### RESULT 25

CCS16068/6  
 LOCUS  
 DEFINITION  
 CH240\_361F11.TARBAC13P2 CHORI-240 Bos taurus genomic clone CH240\_361F11, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

CCS16068.1 GI:31834356  
 GSS.  
 Bos taurus (cow)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 147)  
 Holt, R., Stott, J., Yang, G., Barber, S., Smal, D., Prabhu, A., L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B. P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398  
 Unpublished (2003)  
 Other GSSs: CH240\_361F11.T7  
 Contact: Rob Holt

#### TITLE

#### JOURNAL

#### COMMENT

Sequencing  
 The British Columbia Cancer Agency Genome Science Centre  
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6  
 Tel: 604-877-6085  
 Fax: 604-877-6276  
 Email: rholt@bccsc.ca  
 Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering/information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.  
 Plate: 361 Row: F Column: 11  
 Seq primer: SP6  
 Class: BAC ends.

#### FEATURES

Location/Qualifiers

## source

```

1..147
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_361F11"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

```

## ORIGIN

```

Query Match      100.0%; Score 11; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CTTTGGCACTA 11
    |||||
Db 41 CTTTGGCACTA 31

```

## RESULT 26

```

BM113996
LOCUS      149 bp mRNA linear EST 10-MAR-2003
DEFINITION EST561532 potato roots Solanum tuberosum cDNA clone cPRO2013 5'
end, mRNA sequence.
ACCESSION BM113996
VERSION   BM113996.1 GI:17077044
KEYWORDS
SOURCE    Solanum tuberosum (potato)
ORGANISM  Solanum tuberosum

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 149)
van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
Tanksley,S. and Baker,B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.

```

## REFERENCE

## AUTHORS

## TITLE

```

JOURNAL    Location/Qualifiers
COMMENT    1..149
            /organism="Solanum tuberosum"
            /mol_type="mRNA"
            /cultivar="Kennebec"
            /db_xref="taxon:4113"
            /clone="cPRO2013"
            /tissue_type="roots"
            /dev_stages="in vitro grown stem cuttings"
            /lab_host="SOLR"
            /clone_lib="potato roots"
            /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
            XhoI; supplier: Cornell University, Tanksley lab;
            sequencing; The Institute for Genomic Research. Roots were
            isolated from in vitro grown stem cuttings on CM medium.
            Roots were isolated two weeks after placing the stem
            cuttings from in vitro grown plants on medium."

```

## FEATURES

## source

```

Query Match      100.0%; Score 11; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

## ORIGIN

```

Query Match      100.0%; Score 11; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CTTTGGCACTA 11
    |||||
Db 17 CTTTGGCACTA 27

```

## RESULT 27

```

BM405670
LOCUS      149 bp mRNA linear EST 10-MAR-2003
DEFINITION EST579997 potato roots Solanum tuberosum cDNA clone cPRO24J20 5'
end, mRNA sequence.
ACCESSION BM405670
VERSION   BM405670.1 GI:18257257
KEYWORDS
SOURCE    Solanum tuberosum (potato)
ORGANISM  Solanum tuberosum

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 149)
van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
Tanksley,S. and Baker,B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.

```

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

```

1..149
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPRO24J20"
/tissue_type="roots"
/dev_stages="in vitro grown stem cuttings"
/lab_host="SOLR"
/clone_lib="potato roots"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Cornell University, Tanksley lab;
sequencing; The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."

```

## ORIGIN

```

Query Match      100.0%; Score 11; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CTTTGGCACTA 11
    |||||
Db 17 CTTTGGCACTA 27

```

## RESULT 28

```

R57383/c
LOCUS      150 bp mRNA linear EST 02-MAY-1996
DEFINITION F2971 Fetal heart Homo sapiens cDNA clone F2971 5' end, mRNA
sequence.
ACCESSION R57383
VERSION   R57383.1 GI:827441
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

```

```

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 150)

```



melanogaster cDNA clone EK297249 5, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CO331019  
CO331019.1 GI:49391294  
EST.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 155)

Kopczynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,

Peterson, E. and Swimmer, C.

Exelixis Flytag EST Project CK01 Library

Unpublished (2004)

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu>

Based upon one or more reads of this clone where vector sequence  
was present at both ends, this clone has been determined to contain  
contain a cDNA insert on the order of 600-1000 bases.

Plate: EK.2972 row: E column: 1

High quality sequence stop: 154.

FEATURES  
source

1..155

/organism="Drosophila melanogaster"

/mol\_type="mRNA"

/db\_xref="taxon:7227"

/clone="EK297249"

/note="Organ: mixed stage embryos, imaginal disks, and

adult heads; Vector: pCDNA-SK+; Site\_1: NotI; Site\_2:

XhoI; Random primed, normalized library from mixed stage

embryos, imaginal disks, and adult heads."

ORIGIN

Query Match 100.0%; Score 11; DB 7; Length 155;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

|||||

69 CTTTGGCACTA 79

RESULT 32

CD054495

LOCUS

CD054495 HO1E06r HO Hordeum vulgare cDNA clone HO01E06 5-PRIME, mRNA

156 bp mRNA linear EST 05-JUN-2003

DEFINITION

sequence.

ACCESSION

CD054495

VERSION

CD054495.1 GI:30595488

KEYWORDS

EST.

SOURCE

Hordeum vulgare

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

1 (bases 1 to 156)

Zierold, U. and Schweizer, P.

Barley ESTs from pathogen-attacked leaf epidermis

Unpublished (2003)

Contact: Patrick Schweizer

Transcriptome Analysis, Cytogenetics Department

Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, D-06466 Gatersleben, Germany

Tel: 0049 (0)39482-5660

Fax: 0049 (0)39482-5595

Email: [schweiz@ipk-gatersleben.de](mailto:schweiz@ipk-gatersleben.de)

Insert Length: 156 Std Error: 0.00

Plate: 1 row: E column: 6

FEATURES

source

Seq primer: M13rev.

Location/Qualifiers

1..156

/organism="Hordeum vulgare"

/mol\_type="mRNA"

/cultivar="Ingrid BC mlo-5"

/db\_xref="GABI:703789"

/db\_xref="taxon:4513"

/clone="HO01E06"

/tissue\_type="leaf epidermis, 6 h and 24 h post

inoculation with Blumeria graminis"

/dev\_stage="7 d after germination"

/lab\_host="XL10-Gold"

/clone\_lib="HO"

/note="Vector: pBluescript SK+; Site\_1: EcoRI (5'-end of  
cDNA); Site\_2: XhoI (3'-end of cDNA); Approximately 5 % of  
the clones correspond to cDNA from the fungi B. graminis  
hordei and tritici, respectively. Due to a cloning  
artefact caused by the kit, in most cases the EcoRI site  
is NOT present, as well as the EcoRI adapter used for  
cloning. To excise the insert, restriction sites upstream  
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also  
due to the cloning system used Blue/white selection for  
recombinants is not 100% reliable. Average insert size is  
1.2 kb"

ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 156;

Best Local Similarity 100.0%; Pred. No. 1.7e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

|||||

103 CTTTGGCACTA 113

RESULT 33

BZ654414/c

LOCUS

BZ654414 OGAMR91TM ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMMBma0096014,

genomic survey sequence.

ACCESSION

BZ654414

VERSION

BZ654414.1 GI:28123674

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 156)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OGAMR91TC

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: [whitelaw@tigr.org](mailto:whitelaw@tigr.org)

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..156

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMMBma0096014"

/clone\_lib="ZM 0.7\_1.5\_KB"

/note="Vector: pBGSK-; Site\_1: HincII; 0.7-1.5 kb

## methylation filtered genomic DNA library"

```

ORIGIN
  Query Match      100.0%; Score 11; DB 8; Length 156;
  Best Local Similarity 100.0%; Pred. No. 1.7e+04;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
    |||||
Db 71 CTTTGGCACTA 61

RESULT 34
AV013351
LOCUS
DEFINITION AV013351 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
clone 1110046M18, mRNA sequence.
ACCESSION AV013351
VERSION AV013351.1 GI:4790343
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
Sugahara, Y., Suzuki, H., Suzuki, H., Tatenom, M., Tomaru, Y.,
Tomimaga, N., Watanabe, S., Yagame, M., Yanamura, T., Yokota, T.,
Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES
  source
  Location/Qualifiers
    1..159
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="1110046M18"
    /sex="mixed"
    /dev_stage="18-day embryo"
    /clone_lib="Mus musculus 18-day embryo C57BL/6J"

ORIGIN
  Query Match      100.0%; Score 11; DB 1; Length 159;
  Best Local Similarity 100.0%; Pred. No. 1.7e+04;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
    |||||
Db 2 CTTTGGCACTA 12

RESULT 35
BP671035/c
LOCUS
DEFINITION BP671035 Arabidopsis thaliana cDNA clone RAFL21-37-K01 3',
mRNA sequence.
ACCESSION BP671035
VERSION BP671035.1 GI:49322538
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 162)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
21932900
MEDLINE
PUBMED 11910074
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
  source
  Location/Qualifiers
    1..162
    /organism="Arabidopsis thaliana"
    /mol_type="mRNA"
    /db_xref="taxon:3702"
    /clone="RAFL21-37-K01"
    /lab_host="DH10B"
    /clone_lib="RAFL21"
    /note="Site 1: BamHI; Site 2: SalI; Subtraction Library.
    The sequence was obtained from samples subjected to
    various stress and plant hormones-treated"

ORIGIN
  Query Match      100.0%; Score 11; DB 5; Length 162;
  Best Local Similarity 100.0%; Pred. No. 1.7e+04;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
    |||||
Db 136 CTTTGGCACTA 126

RESULT 36
BH390901
LOCUS
DEFINITION BH390901 162 bp DNA linear GSS 11-DEC-2001
AG-ND-138122.TR ND-TAM Anopheles gambiae genomic clone
AG-ND-138122, genomic survey sequence.
ACCESSION BH390901
VERSION BH390901.1 GI:17337042
KEYWORDS GSS.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae

REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
1 (bases 1 to 162)
Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B.,
Gardner, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
22542063
MEDLINE
PUBMED 12655398

```

COMMENT Other\_GSSs: AG-ND-138L22.TF  
 Contact: Brendan J Loftus  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0208  
 Fax: 301 838 3543  
 Email: bjloftus@tigr.org  
 This clone is from an A. gambiae BAC library (ND-TAM) provided by  
 F.H. Collins and sequenced by The Institute for Genomic Research  
 (TIGR). The BAC library was generated from A. gambiae PEST strain  
 DNA. All DNA was extracted from newly hatched first instar larvae  
 to minimize the inclusion of DNA from microorganisms that inhabit  
 the gut. The DNA is derived from mixed sexes of larvae. The BAC  
 library was constructed at Texas A&M University BAC Center  
 University, College Station, Texas 77843-2123, USA using a HindIII  
 partial digest.  
 Seq primer: M13 Rev  
 Class: BAC ends.

FEATURES source  
 Location/Qualifiers  
 1..162  
 /organism="Anopheles gambiae"  
 /mol\_type="genomic DNA"  
 /strain="PEST"  
 /db\_xref="taxon:7165"  
 /clone="AG-ND-138L22"  
 /clone\_lib="ND-TAM"  
 /note="Vector: pECBAC1; Site\_1: HindIII"

ORIGIN  
 Query Match 100.0%; Score 11; DB 8; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 53 CTTTGGCACTA 63

RESULT 37  
 BW485387 164 bp mRNA linear EST 11-JUN-2004  
 LOCUS  
 DEFINITION BW485387 Nori Satoh unpublished cDNA library, mature adult whole  
 animal Ciona intestinalis cDNA clone cima050g08 5', mRNA sequence.  
 ACCESSION BW485387  
 VERSION  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Cionidae; Ciona.  
 1 (bases 1 to 164)  
 Satou, X., Shin-i, T., Kohara, Y. and Satoh, N.  
 Expressed genes in Ciona intestinalis (2004)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Nori Satoh  
 Department of Zoology  
 Kyoto University  
 Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: satoh@acidian.zool.kyoto-u.ac.jp.

FEATURES source  
 Location/Qualifiers  
 1..164  
 /organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="cima050g08"  
 /tissue\_type="whole animal"  
 /dev\_stage="mature adult"  
 /clone\_lib="Nori Satoh unpublished cDNA library, mature  
 adult whole animal"

ORIGIN

Query Match 100.0%; Score 11; DB 5; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 136 CTTTGGCACTA 146

RESULT 38  
 BZ654404 168 bp DNA linear GSS 29-JAN-2003  
 LOCUS  
 DEFINITION OGAMR91TC ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0096014,  
 genomic survey sequence.  
 ACCESSION BZ654404  
 VERSION BZ654404.1 GI:28123664  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 168)  
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Fraser, C.M., Buddiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
 COMMENT Other\_GSSs: OGAMR91TM  
 Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TF  
 Class: sheared ends.

FEATURES source  
 Location/Qualifiers  
 1..168  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA0096014"  
 /clone\_lib="ZM 0.7 1.5\_KB"  
 /note="Vector: pBCSK-; Site\_1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

ORIGIN  
 Query Match 100.0%; Score 11; DB 8; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 69 CTTTGGCACTA 79

RESULT 39  
 CL954906 168 bp DNA linear GSS 21-SEP-2004  
 LOCUS  
 DEFINITION OsIRUA005118 Oryza sativa Express Library Oryza sativa (indica  
 cultivar-group) genomic, genomic survey sequence.  
 ACCESSION CL954906  
 VERSION CL954906.1 GI:52367015  
 KEYWORDS GSS.  
 SOURCE Oryza sativa (indica cultivar-group)  
 ORGANISM Oryza sativa (indica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 168)

**AUTHORS** Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,  
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,  
Wong,G.K.S., Deng,X.W. and Wang,J.  
**TITLE** An analysis of transcriptional regulation of the rice genome and  
its comparison to Arabidopsis

**JOURNAL** Unpublished (2004)  
**COMMENT** Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.

**FEATURES** Location/Qualifiers  
source  
1..168  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:39946"  
/clone\_lib="Oryza sativa Express Library"  
/note="Oryza sativa exon trapped genomic sequences"

**ORIGIN**  
Query Match 100.0%; Score 11; DB 9; Length 168;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CTTGGGCACTA 11  
|||||  
**Db** 18 CTTGGGCACTA 8

**RESULT 40**  
**CG869416/c**  
**LOCUS** CG869416 172 bp mRNA linear GSS 26-NOV-2003  
**DEFINITION** AE0323 Sanger Institute Gene Trap Library pGT01xr Mus musculus  
cDNA, mRNA sequence.

**ACCESSION** CG869416  
**VERSION** CG869416.1 GI:38533096  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 172)  
**AUTHORS** Sanger Institute Gene Trap Resource - SIGTR.  
**TITLE** http://www.sanger.ac.uk/PostGenomics/genetrap/  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Sanger Institute Gene Trap Resource - SIGTR  
Wellcome Trust Sanger Institute  
Email: info.genetrap@sanger.ac.uk  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from Sanger Institute Gene Trap  
Resource. Annotation information available from  
http://www.sanger.ac.uk/PostGenomics/genetrap/  
Class: Gene Trap.

**FEATURES** Location/Qualifiers  
source  
1..172  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strains="129 OLA"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic Stem Cell"  
/clone\_lib="Sanger Institute Gene Trap Library pGT01xr"  
/note="Vector: pGT01xr"

**ORIGIN**  
Query Match 100.0%; Score 11; DB 9; Length 172;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CTTGGGCACTA 11  
|||||  
**Db** 121 CTTGGGCACTA 111

**RESULT 41**  
**BQ294074/c**  
**LOCUS** BQ294074 174 bp mRNA linear EST 15-MAY-2002  
**DEFINITION** 1091026B01.y2 1091 - Immature ear with common ESTs screened by  
Schmidt lab Zea mays cDNA, mRNA sequence.

**ACCESSION** BQ294074  
**VERSION** BQ294074.1 GI:20803024  
**KEYWORDS** EST.  
**SOURCE** Zea mays  
**ORGANISM** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

**REFERENCE** 1 (bases 1 to 174)  
**AUTHORS** Walbot V.  
**TITLE** Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 1091026 row: B column: 01.

**FEATURES** Location/Qualifiers  
source  
1..174  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/tissue\_type="Inflorescence meristem - floral organ  
primordia"  
/dev\_stage="0.5 cm to 2 cm"  
/lab\_host="Stratagene XL0LR"  
/clone\_lib="1091 - Immature ear with common ESTs screened  
by Schmidt lab"  
/note="Organ: Immature ear; Vector: pAD-GAL4; Site 1:  
EcoRI; Site 2: XhoI; RNA from library 606 was filtered for  
common ESTs found in 606."

**ORIGIN**

Query Match 100.0%; Score 11; DB 5; Length 174;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CTTGGGCACTA 11  
|||||  
**Db** 75 CTTGGGCACTA 65

**RESULT 42**  
**BQ080480**  
**LOCUS** BQ080480 175 bp mRNA linear EST 05-JUL-2004  
**DEFINITION** san33g10.y1 Gm-c1084 Glycine max cDNA clone SOYBEAN CLONE ID:  
Gm-c1084-5708 5', similar to TR:Q9SVES Q9SVES PUTATIVE POLLEN  
ALLERGEN. ;, mRNA sequence.

**ACCESSION** BQ080480  
**VERSION** BQ080480.1 GI:19935539  
**KEYWORDS** EST.  
**SOURCE** Glycine max (soybean)  
**ORGANISM** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.



REFERENCE 1 (bases 1 to 175)  
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.  
 TITLE Public Soybean EST Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 Trace considered overall poor quality  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 1.  
 FEATURES source  
 1..175  
 Location/Qualifiers  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Williams 82"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl084-5708"  
 /tissue\_type="Etolated hypocotyls (Williams 82)"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl084"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed by M. Bhattacharyya from mRNA isolated from etiolated hypocotyls from the cultivar Williams 82. Tissue was inoculated with Phytophthora soyae race 1 and tissues were harvested 2 and 4 hours following infection. The library is the pool of these two time points. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by M. Bhattacharyya in the laboratory of Dr. Randy Shoemaker at Iowa State University."  
 ORIGIN  
 Query Match 100.0%; Score 11; DB 5; Length 175;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTGGCACTA 11  
 |||||  
 Db 120 CTTTGGCACTA 130  
 RESULT 43  
 LOCUS AZ113246/c  
 DEFINITION RPCI-23-475G2-TV RPCI-23 Mus musculus genomic clone RPCI-23-475G2, genomic survey sequence.  
 ACCESSION AZ113246  
 VERSION AZ113246.1 GI:7772594  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 177)

AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.  
 TITLE Mouse BAC End Sequences from Library RPCI-23  
 JOURNAL Unpublished (1999)  
 COMMENT Other GSSs: RPCI-23-475G2.TJ  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tldb/bac\_ends/mouse/bac\_end\_intro.html  
 Plate: 475 row: G column: 2  
 Seq primer: T7  
 Class: BAC ends.  
 FEATURES source  
 1..177  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-475G2"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /clone\_lib="RPCI-23"  
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."  
 ORIGIN  
 Query Match 100.0%; Score 11; DB 8; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTGGCACTA 11  
 |||||  
 Db 73 CTTTGGCACTA 63  
 RESULT 44  
 LOCUS AA065630/c  
 DEFINITION mm42ell.r1 Stragatene mouse melanoma (#937312) Mus musculus CDNA clone IMAGE:524204 5', mRNA sequence.  
 ACCESSION AA065630  
 VERSION AA065630.1 GI:1563210  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 178)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:318052  
Seq primer: -28ml3 rev1 ET from Amersham  
High quality sequence stop: 160.  
Location/Qualifiers  
1. 178  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:524204"  
/tissue\_type="melanoma"  
/dev\_stage="M2 cells"  
/lab\_host="SOLR (kanamycin resistant)"  
/clone\_lib="Stratagene mouse melanoma (#937312)"  
/note="Organ: skin; Vector: pBluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dt. From M2 cells, a highly metastatic derivative of  
the K-1735 (mouse) melanoma. Average insert size: 1.0 kb;  
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGACGAG  
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN  
Query Match 100.0%; Score 11; DB 1; Length 178;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTGGCACTA 11  
|||||  
Db 134 CTTTGGCACTA 124

RESULT 45  
BM829109/c  
LOCUS  
DEFINITION BM829109 178 bp mRNA linear EST 06-MAR-2002  
K-EST0102035 S9SNU601 Homo sapiens cDNA clone S9SNU601-56-A12 5',  
mRNA sequence.  
ACCESSION BM829109  
VERSION BM829109.1 GI:19185518  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 56 row: A column: 12  
High quality sequence stop: 178.  
Location/Qualifiers  
1. 178  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S9SNU601-56-A12"  
/sex="M"  
/tissue\_type="Ascites"  
/cell\_type="Epithelial"  
/cell\_line="SNU-601"

ORIGIN  
Query Match 100.0%; Score 11; DB 1; Length 178;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTGGCACTA 11  
|||||  
Db 134 CTTTGGCACTA 124

RESULT 46  
BM406539/c  
LOCUS  
DEFINITION BM406539 Yutaka Satou unpublished cDNA library, embryo whole animal  
Ciona intestinalis cDNA clone ciem851106 3', mRNA sequence.  
ACCESSION BM406539  
VERSION BM406539.1 GI:47822367  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Satou,Y., Shin,I.T., Kohara,Y. and Satoh,N.  
JOURNAL Expressed genes in Ciona intestinalis (2004)  
COMMENT Unpublished (2004)  
Contact: Yutaka Satou  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4095  
Fax: 81-75-705-1113  
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers  
1. 178  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="ciem851106"  
/tissue\_type="whole animal"  
/dev\_stage="embryo"  
/clone\_lib="Yutaka Satou unpublished cDNA library, embryo  
whole animal"

ORIGIN  
Query Match 100.0%; Score 11; DB 5; Length 178;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTGGCACTA 11  
|||||  
Db 111 CTTTGGCACTA 101

RESULT 47  
BM829109/c  
LOCUS  
DEFINITION BM829109 178 bp mRNA linear EST 06-MAR-2002  
K-EST0102035 S9SNU601 Homo sapiens cDNA clone S9SNU601-56-A12 5',  
mRNA sequence.  
ACCESSION BM829109  
VERSION BM829109.1 GI:19185518  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 56 row: A column: 12  
High quality sequence stop: 178.  
Location/Qualifiers  
1. 178  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S9SNU601-56-A12"  
/sex="M"  
/tissue\_type="Ascites"  
/cell\_type="Epithelial"  
/cell\_line="SNU-601"

ORIGIN  
Query Match 100.0%; Score 11; DB 5; Length 178;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTTGGCACTA 11  
|||||  
Db 111 CTTTGGCACTA 101

```

CE643587
LOCUS      CE643587      180 bp      DNA      linear      GSS 29-SEP-2003
DEFINITION tigr-gss-dog-17000366885068 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION  CE643587
VERSION    CE643587.1  GI:36961833
KEYWORDS   GSS.
SOURCE     Canis familiaris (dog)
ORGANISM   Canis familiaris
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
            1 (bases 1 to 180)
            Kirchner, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,
            Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
            Venter, J.C.
            The dog genome: survey sequencing and comparative analysis
            Science 301 (5641), 1898-1903 (2003)
            22875432
            14512627
            Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
            Location/Qualifiers
            1..180
            /organism="Canis familiaris"
            /mol_type="genomic DNA"
            /strain="Standard Poodle"
            /db_xref="taxon:9615"
            /clone_lib="Dog Library"
            /note="Site 1: BSK1; Libraries were prepared from
            peripheral blood"

ORIGIN
Query Match      100.0%; Score 11; DB 9; Length 180;
Best Local Similarity 100.0%; Pred.No. 1.7e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CTTTGGCACTA 11
        |||||
        101 CTTTGGCACTA 111

Db

RESULT 48
BM110364
LOCUS      BM110364      181 bp      mRNA      linear      EST 10-MAR-2003
DEFINITION EST557900 potato roots Solanum tuberosum cDNA clone cPRO7P9 5' end,
            mRNA sequence.
ACCESSION  BM110364
VERSION    BM110364.1  GI:17072035
KEYWORDS   EST.
SOURCE     Solanum tuberosum (potato)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiales; Solanales; Solanaceae; Solanum.
            1 (bases 1 to 181)
            Van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
            Uterback, T., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C.,
            Tanksley, S. and Baker, B.
            Generation of ESTs from potato roots
            Unpublished (2001)
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/

FEATURES
source
1..180
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPRO7P9"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
/clone_lib="potato roots"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Cornell University, Tanksley lab;
sequencing: The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."

ORIGIN
Query Match      100.0%; Score 11; DB 4; Length 181;
Best Local Similarity 100.0%; Pred.No. 1.7e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CTTTGGCACTA 11
        |||||
        17 CTTTGGCACTA 27

Db

RESULT 49
CF206632
LOCUS      CF206632      181 bp      mRNA      linear      EST 04-AUG-2003
DEFINITION RR890915I0007 IIIC Rc H08 Vitis sp. RR890915I Vitis hybrid cultivar
            CDNA clone RR890915I0007 IIIC Rc_H08 3', mRNA sequence.
ACCESSION  CF206632
VERSION    CF206632.1  GI:33401005
KEYWORDS   EST.
SOURCE     Vitis hybrid cultivar
ORGANISM   Vitis hybrid cultivar
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
            1 (bases 1 to 181)
            Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
            Jones, K. and Cook, D.
            Transcriptional responses of a Pierce's Disease resistant Vitis sp.
            to infection by Xylella fastidiosa
            Unpublished (2003)
            Contact: Douglas Cook, PhD
            CAES Genome Facility
            UC Davis, Plant Pathology
            One Shields Ave, Davis, CA 95616, USA
            Tel: 530 754 6561
            Fax: 530 754 6617
            Email: drcook@ucdavis.edu
            Seq primer: GCCAAACGAATGCTCTAG.

FEATURES
source
1..181
/organism="Vitis hybrid cultivar"
/mol_type="mRNA"
/db_xref="taxon:241073"
/clone="RR890915I0007 IIIC Rc_H08"
/lab_host="DH5alpha"
/clone_lib="Vitis sp. RR890915I"
/note="Organ: Leaf; Vector: pDNR; Site 1: SfiI; Site 2:
SfiI; RR890915I is a cDNA library of leaves from the F1 of
Vitis rupestris 'A. de Serres' x V. spp. 'b42-26'
(8909-15) showing resistance to Xylella fastidiosa under
greenhouse experimental conditions (M. Andrew Walker and
Alan Krivanek, U C Davis). Samples were collected from
17-week old greenhouse grown plants, nine weeks after
inoculation with the bacterial pathogen Xylella
fastidiosa. cDNAs were made by oligo-dT priming and

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directionally cloned. 5' and 3' adaptors were used in cloning as follows:  
5'-RAGCAGTGGTATCAGCAGAGTGGCCATTACGGCCGG-3' and  
5'-ATTCTAGAGCGGAGCGCCGACATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

## ORIGIN

Query Match 100.0%; Score 11; DB 7; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
DB 41 CTTTGGCACTA 51

RESULT 50  
BM748955/c  
LOCUS BM748955 182 bp mRNA linear EST 04-MAR-2002  
DEFINITION K-EST0024004 S2SNU668 Homo sapiens cDNA clone S2SNU668-2-G06 5',  
mRNA sequence.  
ACCESSION BM748955  
VERSION BM748955.1 GI:19078573  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 182)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001  
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Plate: 2 row: G column: 06  
High quality sequence stop: 182.

## FEATURES

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/cell\_line="SNU-668"  
/lab\_host="Top10P"  
/clone\_lib="S2SNU668"  
/note="Organ: Stomach; Vector: pcms; Site\_1: EcoRI;  
Site\_2: NotI; The poly (A)+ RNA was decapped with tobacco  
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker  
including EcoRI site by treatment of T4 RNA ligase. The  
first strand cDNA was synthesized from oligo dt-selected  
mRNA by priming with dt-tailed vector. The dt-tailed  
vector was adjusted to have about 60nt. The cDNA vector  
was circularized with E. coli DNA ligase after digestion  
of EcoRI which site is also included in vector. An RNA  
strand converted to a DNA strand by Okayama-Berg method.  
The obtained cDNA vectors were used for transfection of  
competent cells E. coli Top10P' by electroporation  
method."

## ORIGIN

Query Match 100.0%; Score 11; DB 4; Length 182;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTGGCACTA 11  
|||||  
DB 141 CTTTGGCACTA 131

Search completed: March 12, 2005, 10:58:15  
Job time : 1792 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 07:19:17 ; Search time 1429 Seconds  
(without alignments)  
372.993 Million cell updates/sec

Title: US-10-070-588A-112  
Perfect score: 11  
Sequence: 1 ctttggcacta 11

Scoring table: OLIGO NUC  
Gapop 50.0 , Gapext 50.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_scs: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	11	100.0	11	6	AX099050 Sequence
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6	11	100.0	47	6	AX427666 Sequence
7	11	100.0	77	6	CQ057099 Sequence
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11	11	100.0	77	6	CQ205816 Sequence
12	11	100.0	77	6	CQ229223 Sequence
13	11	100.0	77	6	CQ267352 Sequence
14	11	100.0	77	6	CQ304373 Sequence
15	11	100.0	77	6	CQ341641 Sequence
16	11	100.0	100	6	AX310296 Sequence
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18	11	100.0	121	6	AX325267 Sequence
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53	11	100.0	251	11	BV084047	BV084047 sc1275_p3
c 54	11	100.0	252	8	CUSCC	D63386 Cucumis sat
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c 137	11	100.0	354	14	AF455806	AF455806 Vaccinia	c 210	11	100.0	449	11	G70149	G70149 713500831FO
c 138	11	100.0	355	6	CQ485573	CQ485573 Sequence	c 211	11	100.0	449	14	AY049756	AY049756 Human pap
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C 251	11	100.0	468	6	CQ702226	CQ702226 Sequence	324	11	100.0	545	6	CQ672262	CQ672262 Sequence
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C 253	11	100.0	472	6	CQ418458	CQ418458 Sequence	C 326	11	100.0	545	11	G77971	G77971 S209P6159RC
C 254	11	100.0	472	6	CQ426228	CQ426228 Sequence	327	11	100.0	546	11	G81755	G81755 S210P6249FD
C 255	11	100.0	472	6	CQ681596	CQ681596 Sequence	328	11	100.0	546	11	G83271	G83271 S210P6121RG
C 256	11	100.0	472	9	S78684S2	S78685 Homo sapien	C 329	11	100.0	549	8	AF186632	AF186632 Pennisetu
C 257	11	100.0	474	6	CQ698653	CQ698653 Sequence	330	11	100.0	550	11	G69766	G69766 713500831FB
C 258	11	100.0	474	11	G71155	G71155 713510831FM	C 331	11	100.0	551	6	AR255909	AR255909 Sequence
C 259	11	100.0	475	6	AR414421	AR414421 Sequence	C 332	11	100.0	551	6	AX040589	AX040589 Sequence
C 260	11	100.0	475	6	AX971255	AX971255 Sequence	333	11	100.0	551	11	G69598	G69598 713510831FB
C 261	11	100.0	475	6	BD109974	BD109974 EST and e	334	11	100.0	552	6	AR395114	AR395114 Sequence
C 262	11	100.0	477	1	AV236466	AV236466 Anaplasma	335	11	100.0	552	11	G69999	G69999 713500831FN
C 263	11	100.0	477	6	AR547771	AR547771 Sequence	C 336	11	100.0	552	11	G70045	G70045 713500831FN
C 264	11	100.0	478	6	CQ054320	CQ054320 Sequence	C 337	11	100.0	553	1	U97483	U97483 Rickettsia
C 265	11	100.0	478	6	CQ073557	CQ073557 Sequence	338	11	100.0	554	6	AX241774	AX241774 Sequence
C 266	11	100.0	478	6	CQ104439	CQ104439 Sequence	339	11	100.0	554	11	G69968	G69968 713500831FN
C 267	11	100.0	478	6	CQ143158	CQ143158 Sequence	C 340	11	100.0	555	11	BV055859	BV055859 S212P6025
C 268	11	100.0	478	6	CQ178643	CQ178643 Sequence	C 341	11	100.0	559	11	BV187892	BV187892 sqmm15569
C 269	11	100.0	478	6	CQ202992	CQ202992 Sequence	342	11	100.0	560	11	BV112139	BV112139 PZAO1681
C 270	11	100.0	478	6	CQ226339	CQ226339 Sequence	C 343	11	100.0	561	6	CQ528465	CQ528465 Sequence
C 271	11	100.0	478	6	CQ264481	CQ264481 Sequence	C 344	11	100.0	563	1	VCH231075	AVJ231075 Vibrio ch
C 272	11	100.0	478	6	CQ301576	CQ301576 Sequence	C 345	11	100.0	565	6	AX400375	AX400375 Sequence
C 273	11	100.0	478	6	CQ338791	CQ338791 Sequence	C 346	11	100.0	570	6	AR303079	AR303079 Sequence
C 274	11	100.0	480	9	F461712S03	AF461714 Homo sapi	C 347	11	100.0	570	8	AF126818	AF126818 Ampelomyc
C 275	11	100.0	481	6	CQ052847	CQ052847 Sequence	348	11	100.0	575	6	CQ776485	CQ776485 Sequence
C 276	11	100.0	481	6	CQ067935	CQ067935 Sequence	349	11	100.0	576	6	CQ072596	CQ072596 Sequence
C 277	11	100.0	481	6	CQ094989	CQ094989 Sequence	350	11	100.0	576	6	CQ103407	CQ103407 Sequence
C 278	11	100.0	481	6	CQ216977	CQ216977 Sequence	351	11	100.0	576	6	CQ142241	CQ142241 Sequence
C 279	11	100.0	481	11	G69688	G69688 713500831FB	C 352	11	100.0	577	11	BV112148	BV112148 PZAO1681
C 280	11	100.0	481	13	AX713443	AX713443 Unculture	C 353	11	100.0	579	11	BV112145	BV112145 PZAO1681
C 281	11	100.0	485	11	BV005736	BV005736 BARC0002	C 354	11	100.0	580	6	AX387326	AX387326 Sequence
C 282	11	100.0	486	6	CQ479618	CQ479618 Sequence	355	11	100.0	582	11	BV112147	BV112147 PZAO1681
C 283	11	100.0	487	11	G70293	G70293 713510831FB	C 356	11	100.0	582	11	BV112143	BV112143 PZAO1681
C 284	11	100.0	487	11	G70686	G70686 713510831FB	C 357	11	100.0	582	11	BV112146	BV112146 PZAO1681
C 285	11	100.0	489	6	CQ528155	CQ528155 Sequence	C 358	11	100.0	583	11	BV112135	BV112135 PZAO1681
C 286	11	100.0	490	11	G69931	G69931 713510831FN	C 359	11	100.0	583	11	BV112141	BV112141 PZAO1681
C 287	11	100.0	493	1	AF508017	AF508017 Helicobac	C 360	11	100.0	584	11	G87470	G87470 S208P6755FF
C 288	11	100.0	495	6	CQ524379	CQ524379 Sequence	361	11	100.0	585	11	BV112144	BV112144 PZAO1681
C 289	11	100.0	498	1	AY112687	AY112687 Anaplasma	C 362	11	100.0	586	9	AY027772	AY027772 Homo sapi
C 290	11	100.0	505	6	AR424178	AR424178 Sequence	C 363	11	100.0	590	6	CQ225167	CQ225167 Sequence
C 291	11	100.0	505	6	AX984872	AX984872 Sequence	C 364	11	100.0	590	6	CQ337472	CQ337472 Sequence
C 292	11	100.0	505	6	BD119731	BD119731 EST and e	C 365	11	100.0	593	11	BV112140	BV112140 PZAO1681
C 293	11	100.0	508	11	BV077085	BV077085 S212P6146	366	11	100.0	595	11	BV112138	BV112138 PZAO1681
C 294	11	100.0	518	11	G70084	G70084 713500831FN	C 367	11	100.0	595	11	BV112136	BV112136 PZAO1681
C 295	11	100.0	519	11	G69959	G69959 713510831FB	C 368	11	100.0	599	11	G99545	G99545 S208P6725RF
C 296	11	100.0	519	11	G69992	G69992 713510831FN	C 369	11	100.0	601	11	BV112133	BV112133 PZAO1681
C 297	11	100.0	524	11	G70117	G70117 713500831FN	370	11	100.0	601	11	BV112142	BV112142 PZAO1681
C 298	11	100.0	525	6	CQ519452	CQ519452 Sequence	371	11	100.0	601	11	BV112143	BV112143 PZAO1681
C 299	11	100.0	528	6	CQ737175	CQ737175 Sequence	C 372	11	100.0	602	11	BV179796	BV179796 sqmm16676
C 300	11	100.0	528	11	G69606	G69606 713500831FB	373	11	100.0	602	11	BV055978	BV055978 S212P6167
C 301	11	100.0	528	11	G69644	G69644 713510831FB	374	11	100.0	603	11	BV112134	BV112134 PZAO1681
C 302	11	100.0	528	11	G70398	G70398 713510831FV	375	11	100.0	603	11	BV112137	BV112137 PZAO1681
C 303	11	100.0	530	9	AY027773	AY027773 Homo sapi	C 376	11	100.0	611	11	BV161559	BV161559 RPAMMSQ0
C 304	11	100.0	531	6	G90298	G90298 S210P6050F6	377	11	100.0	615	3	AY081769	AY081769 Bombyx mo
C 305	11	100.0	531	6	AX361027	AX361027 Sequence	C 378	11	100.0	618	14	HPCNS2PA	MS5971 Hepatitis C
C 306	11	100.0	531	6	AX377693	AX377693 Sequence	379	11	100.0	623	6	BD193991	BD193991 Enterococ
C 307	11	100.0	531	11	BV209964	BV209964 ZETB10 4	380	11	100.0				
C 308	11	100.0	532	8	AK102011	AK102011 Oryza sat	381	11	100.0				
C 309	11	100.0	532	8	AK102011	AK102011 Oryza sat	382	11	100.0				
C 310	11	100.0	534	11	G52650	G52650 SHGC-85705	383	11	100.0				
C 311	11	100.0	535	11	G69651	G69651 713500831FB	C 384	11	100.0				

C 385	11	100.0	627	6	AX387353 Sequence	AX387353 Sequence	C 458	11	100.0	795	3	AY451312 Echinomet
C 386	11	100.0	631	11	BV022323 S212P6044	BV022323 S212P6044	C 459	11	100.0	798	3	AY451311 Echinomet
C 387	11	100.0	634	6	AX387354 Sequence	AX387354 Sequence	C 460	11	100.0	799	5	AY509834 Scardinu
C 388	11	100.0	635	6	CQ523393 Sequence	CQ523393 Sequence	C 461	11	100.0	799	11	BV166430 KCNU6_880
C 389	11	100.0	636	6	AX400546 Sequence	AX400546 Sequence	C 462	11	100.0	801	6	AX275459 Solanum d
C 390	11	100.0	637	3	AF153749 Sepia off	AF153749 Sepia off	C 463	11	100.0	806	6	AX393325 Sequence
C 391	11	100.0	641	11	BV018433 S212P6035	BV018433 S212P6035	C 464	11	100.0	807	3	AY451275 Echinomet
C 392	11	100.0	654	11	G06154 human SFS	G06154 human SFS	C 465	11	100.0	810	3	AY451250 Echinomet
C 393	11	100.0	657	11	BV022841 S212P6115	BV022841 S212P6115	C 466	11	100.0	810	11	BV208788 RAB9B_254
C 394	11	100.0	660	9	HSRPL18AH	X80821 H.sapiens m	C 467	11	100.0	812	6	BD192944 207 human
C 395	11	100.0	660	11	BV078357 px-6c7 Fl	BV078357 px-6c7 Fl	C 468	11	100.0	812	6	CQ821940 Sequence
C 396	11	100.0	668	6	AX255881 Sequence	AX255881 Sequence	C 469	11	100.0	813	3	AY451274 Echinomet
C 397	11	100.0	678	6	AR395115 Sequence	AR395115 Sequence	C 470	11	100.0	813	6	BD148503 Primer fo
C 398	11	100.0	678	11	BV022592 S212P6043	BV022592 S212P6043	C 471	11	100.0	813	6	AX868441 Sequence
C 399	11	100.0	683	8	AF443179 Nicotiana	AF443179 Nicotiana	C 472	11	100.0	814	14	AF004463 Venezuela
C 400	11	100.0	693	3	EMU39507 Echinometra	U39507 Echinometra	C 473	11	100.0	816	3	AY451307 Echinomet
C 401	11	100.0	699	3	EMU39508 Echinometra	U39508 Echinometra	C 474	11	100.0	816	3	AY451315 Echinomet
C 402	11	100.0	705	11	BV044499 S212P6637	BV044499 S212P6637	C 475	11	100.0	816	6	AR449375 Sequence
C 403	11	100.0	706	9	HSR339642 Homo sapi	AJ339642 Homo sapi	C 476	11	100.0	819	3	AY451272 Echinomet
C 404	11	100.0	711	3	EMU39509 Echinometra	U39509 Echinometra	C 477	11	100.0	819	3	AY451273 Echinomet
C 405	11	100.0	711	3	EMU39511 Echinometra	U39511 Echinometra	C 478	11	100.0	822	3	AY451251 Echinomet
C 406	11	100.0	720	3	EMU39512 Echinometra	AY451283 Echinomet	C 479	11	100.0	822	3	AY451261 Echinomet
C 407	11	100.0	722	6	AX525797 Sequence	AX525797 Sequence	C 480	11	100.0	822	3	AY451309 Echinomet
C 408	11	100.0	724	14	HCU37610 Hepatitis C	U37610 Hepatitis C	C 481	11	100.0	824	8	AY333925 Antirrhin
C 409	11	100.0	724	14	HCU37611 Hepatitis C	U37611 Hepatitis C	C 482	11	100.0	825	3	AY451262 Echinomet
C 410	11	100.0	724	14	HCU37612 Hepatitis C	U37612 Hepatitis C	C 483	11	100.0	825	3	AY451308 Echinomet
C 411	11	100.0	724	14	HCU37624 Hepatitis C	U37624 Hepatitis C	C 484	11	100.0	826	3	AY451310 Echinomet
C 412	11	100.0	724	14	HCU37625 Hepatitis C	U37625 Hepatitis C	C 485	11	100.0	826	3	AY451265 Echinomet
C 413	11	100.0	724	14	HCU37626 Hepatitis C	U37626 Hepatitis C	C 486	11	100.0	828	3	AY451243 Echinomet
C 414	11	100.0	724	14	HCU37627 Hepatitis C	U37627 Hepatitis C	C 487	11	100.0	828	3	AY451246 Echinomet
C 415	11	100.0	724	14	HCU37631 Hepatitis C	U37631 Hepatitis C	C 488	11	100.0	828	3	AY451247 Echinomet
C 416	11	100.0	726	3	EOU39502 Echinometra	U39502 Echinometra	C 489	11	100.0	828	3	AY451252 Echinomet
C 417	11	100.0	726	3	EOU39503 Echinometra	U39503 Echinometra	C 490	11	100.0	828	3	AY451253 Echinomet
C 418	11	100.0	729	3	EOU39506 Echinometra	U39506 Echinometra	C 491	11	100.0	828	3	AY451255 Echinomet
C 419	11	100.0	731	11	BV012435 ORS 167 S	BV012435 ORS 167 S	C 492	11	100.0	828	3	AY451256 Echinomet
C 420	11	100.0	733	11	BV122394 PZA01695	BV122394 PZA01695	C 493	11	100.0	828	3	AY451257 Echinomet
C 421	11	100.0	734	11	BV122397 PZA01695	BV122397 PZA01695	C 494	11	100.0	828	3	AY451258 Echinomet
C 422	11	100.0	735	11	BV122405 PZA01695	BV122405 PZA01695	C 495	11	100.0	828	3	AY451260 Echinomet
C 423	11	100.0	736	11	BV122393 PZA01695	BV122393 PZA01695	C 496	11	100.0	828	3	AY451263 Echinomet
C 424	11	100.0	736	11	BV122400 PZA01695	BV122400 PZA01695	C 497	11	100.0	828	3	AY451266 Echinomet
C 425	11	100.0	737	11	BV122403 PZA01695	BV122403 PZA01695	C 498	11	100.0	828	3	AY451267 Echinomet
C 426	11	100.0	737	11	BV122395 PZA01695	BV122395 PZA01695	C 499	11	100.0	828	3	AY451316 Echinomet
C 427	11	100.0	738	11	BV122402 PZA01695	BV122402 PZA01695	C 500	11	100.0	831	3	AY451269 Echinomet
C 428	11	100.0	738	11	BV122404 PZA01695	BV122404 PZA01695	C 501	11	100.0	831	3	AY451318 Echinomet
C 429	11	100.0	739	11	BV122391 PZA01695	BV122391 PZA01695	C 502	11	100.0	831	3	AY451319 Echinomet
C 430	11	100.0	739	11	BV122392 PZA01695	BV122392 PZA01695	C 503	11	100.0	831	3	AY451321 Echinomet
C 431	11	100.0	739	11	BV122399 PZA01695	BV122399 PZA01695	C 504	11	100.0	831	3	AY451322 Echinomet
C 432	11	100.0	740	11	BV122396 PZA01695	BV122396 PZA01695	C 505	11	100.0	834	3	AY451323 Echinomet
C 433	11	100.0	740	11	BV122398 PZA01695	BV122398 PZA01695	C 506	11	100.0	834	3	AY451242 Echinomet
C 434	11	100.0	740	11	BV122406 PZA01695	BV122406 PZA01695	C 507	11	100.0	834	3	AY451270 Echinomet
C 435	11	100.0	741	11	BV122401 PZA01695	BV122401 PZA01695	C 508	11	100.0	834	3	AY451271 Echinomet
C 436	11	100.0	750	6	AR454846 Sequence	AR454846 Sequence	C 509	11	100.0	834	3	AY451286 Echinomet
C 437	11	100.0	750	6	AX427661 Sequence	AX427661 Sequence	C 510	11	100.0	834	3	AY451289 Echinomet
C 438	11	100.0	753	3	ESU39514 Echinometra	U39514 Echinometra	C 511	11	100.0	834	3	AY451317 Echinomet
C 439	11	100.0	759	6	AX414092 Sequence	AX414092 Sequence	C 512	11	100.0	837	3	AY451249 Echinomet
C 440	11	100.0	761	6	AR494922 Sequence	AR494922 Sequence	C 513	11	100.0	837	3	AY451259 Echinomet
C 441	11	100.0	761	8	AF378056 Sequence	AF378056 Sequence	C 514	11	100.0	837	3	AY451288 Echinomet
C 442	11	100.0	762	6	CQ740543 Sequence	CQ740543 Sequence	C 515	11	100.0	837	3	AY451297 Echinomet
C 443	11	100.0	762	8	AF378039 Lycopersi	AF378039 Lycopersi	C 516	11	100.0	837	3	AY451304 Echinomet
C 444	11	100.0	762	8	AR494926 Sequence	AR494926 Sequence	C 517	11	100.0	840	3	AY451320 Echinomet
C 445	11	100.0	763	6	AR494926 Sequence	AR494926 Sequence	C 518	11	100.0	840	3	AY451245 Echinomet
C 446	11	100.0	763	8	AF378060 Sorghum b	AF378060 Sorghum b	C 519	11	100.0	840	3	AY451282 Echinomet
C 447	11	100.0	768	3	AY451284 Echinomet	AY451284 Echinomet	C 520	11	100.0	841	8	AB026440 Nicotiana
C 448	11	100.0	768	11	BV058545 S212P6600	BV058545 S212P6600	C 521	11	100.0	842	11	BV068299 S212P6051
C 449	11	100.0	771	6	BD149264 Primer fo	BD149264 Primer fo	C 522	11	100.0	843	3	AY451244 Echinomet
C 450	11	100.0	771	6	AX869202 Sequence	AX869202 Sequence	C 523	11	100.0	843	3	AY451248 Echinomet
C 451	11	100.0	773	3	LIN275321 Lefshmani	AJ275321 Lefshmani	C 524	11	100.0	843	3	AY451254 Echinomet
C 452	11	100.0	786	6	CQ728376 Sequence	CQ728376 Sequence	C 525	11	100.0	843	3	AY451279 Echinomet
C 453	11	100.0	787	6	AR354238 Sequence	AR354238 Sequence	C 526	11	100.0	843	3	AY451292 Echinomet
C 454	11	100.0	787	6	AR535794 Sequence	AR535794 Sequence	C 527	11	100.0	843	3	AY451293 Echinomet
C 455	11	100.0	787	10	L47300S11 Rattus norv	L47300 Rattus norv	C 528	11	100.0	843	3	AY451305 Echinomet
C 456	11	100.0	789	8	AB010953 Torenia f	AB010953 Torenia f	C 529	11	100.0	843	3	AY451313 Echinomet
C 457	11	100.0	793	11	BV033512 S212P6625	BV033512 S212P6625	C 530	11	100.0	843	3	AY451314 Echinomet



C 531	11	100.0	843	6	CQ740805	Sequence	C 604	11	100.0	1053	6	AX489452	Sequence
C 532	11	100.0	846	3	AY451268	Echinomet	C 605	11	100.0	1059	6	AR123363	Sequence
C 533	11	100.0	846	3	AY451281	Echinomet	C 606	11	100.0	1065	6	CQ803816	Sequence
C 534	11	100.0	847	6	I44710	Sequence 20	607	11	100.0	1071	6	AX570144	Sequence
C 535	11	100.0	847	6	I52116	Sequence 20	608	11	100.0	1072	5	CR353032	Sequence
C 536	11	100.0	849	3	AY451264	Echinomet	C 609	11	100.0	1074	6	I44702	Sequence 4
C 537	11	100.0	852	11	BV015079	Sequence	C 610	11	100.0	1074	6	I52108	Sequence 4
C 538	11	100.0	855	3	AY451278	Echinomet	C 611	11	100.0	1074	6	AR479673	Sequence
C 539	11	100.0	855	3	AY451280	Echinomet	C 612	11	100.0	1076	6	I44700	Sequence 1
C 540	11	100.0	858	3	AY451290	Echinomet	C 613	11	100.0	1076	6	I52106	Sequence 1
C 541	11	100.0	858	3	AY451291	Echinomet	C 614	11	100.0	1076	6	AR364044	Sequence
C 542	11	100.0	863	5	BR9331637	Callus ga	C 615	11	100.0	1076	8	MZERIP	Sequence
C 543	11	100.0	863	6	BD206392	Human nuc	C 616	11	100.0	1077	5	AR383548	Pleurodel
C 544	11	100.0	863	6	AR400707	Sequence	617	11	100.0	1083	6	AR395092	Sequence
C 545	11	100.0	863	6	AX013597	Sequence	618	11	100.0	1092	8	STENCHIT	Sequence
C 546	11	100.0	865	14	MLVTRPD	Y07808 MLV-related	619	11	100.0	1092	14	AF014959	Hepatitis
C 547	11	100.0	866	6	BD079677	Cancer-as	620	11	100.0	1097	8	AF043248	Solanum t
C 548	11	100.0	870	3	AY451294	Echinomet	C 621	11	100.0	1098	5	CR408251	Callus ga
C 549	11	100.0	870	3	AY451295	Echinomet	622	11	100.0	1100	8	STU02607	Solanum tub
C 550	11	100.0	870	3	AY451296	Echinomet	623	11	100.0	1100	6	AX003309	Sequence
C 551	11	100.0	870	3	AY451298	Echinomet	C 624	11	100.0	1105	6	I44701	Sequence 3
C 552	11	100.0	870	3	AY451300	Echinomet	C 625	11	100.0	1105	6	I52107	Sequence 3
C 553	11	100.0	879	6	CO643964	Sequence	C 626	11	100.0	1105	6	AR364045	Sequence
C 554	11	100.0	880	6	BD060507	Secreted	C 627	11	100.0	1108	8	AF043247	Solanum t
C 555	11	100.0	882	3	AY451276	Echinomet	C 628	11	100.0	1117	6	CQ722054	Sequence
C 556	11	100.0	882	3	AY451302	Echinomet	C 629	11	100.0	1125	6	AR395398	Sequence
C 557	11	100.0	882	5	BR930353	Callus ga	630	11	100.0	1130	14	HPCPVGP	Sequence
C 558	11	100.0	882	6	AX608099	Sequence	631	11	100.0	1140	4	AV170112	Viverra t
C 559	11	100.0	885	3	AY451277	Echinomet	632	11	100.0	1140	5	AY509833	Scardinu
C 560	11	100.0	885	3	AY451303	Echinomet	633	11	100.0	1140	5	AY509835	Scardinu
C 561	11	100.0	885	3	AY451306	Echinomet	634	11	100.0	1140	5	AY509836	Scardinu
C 562	11	100.0	888	3	AY451285	Echinomet	635	11	100.0	1140	5	AY509837	Scardinu
C 563	11	100.0	907	8	STU02608	Solanum tub	636	11	100.0	1140	5	AY509838	Scardinu
C 564	11	100.0	909	6	AX427660	Sequence	637	11	100.0	1140	5	AY509839	Scardinu
C 565	11	100.0	910	6	EO6891	DNA encodin	638	11	100.0	1140	5	AY509840	Scardinu
C 566	11	100.0	913	3	AX522440	Lepeophth	639	11	100.0	1140	5	AY509841	Scardinu
C 567	11	100.0	920	6	AX277145	Sequence	640	11	100.0	1140	5	AY509842	Scardinu
C 568	11	100.0	924	1	SMU26731	Sequence	641	11	100.0	1140	5	AY509843	Scardinu
C 569	11	100.0	924	8	AB026439	Nicotiana	642	11	100.0	1140	5	AY509844	Scardinu
C 570	11	100.0	944	6	AR123368	Sequence	643	11	100.0	1140	5	AY509845	Scardinu
C 571	11	100.0	951	8	AF197330	Eucalyptu	644	11	100.0	1140	5	AY509846	Scardinu
C 572	11	100.0	951	8	AF197334	Eucalyptu	645	11	100.0	1140	5	AY509847	Scardinu
C 573	11	100.0	959	8	ZMA300265	Zea mays	646	11	100.0	1140	5	AY509848	Scardinu
C 574	11	100.0	960	6	CQ414733	Sequence	647	11	100.0	1140	5	AY509848	Scardinu
C 575	11	100.0	963	8	MZERIP2A	Sequence	C 648	11	100.0	1161	6	I44707	Sequence 14
C 576	11	100.0	978	6	I44705	Sequence 10	C 649	11	100.0	1161	6	I52113	Sequence 14
C 577	11	100.0	978	6	I52111	Sequence 10	C 650	11	100.0	1164	6	CQ805740	Sequence
C 578	11	100.0	983	8	AF233881	Zea mays	C 651	11	100.0	1167	8	AK061061	Oryza sat
C 579	11	100.0	985	6	I44704	Sequence 8	C 652	11	100.0	1175	8	AF178951	Zea mays
C 580	11	100.0	985	6	I52110	Sequence 8	C 653	11	100.0	1185	6	AR506487	Sequence
C 581	11	100.0	985	9	BC004308	Homo sapi	C 654	11	100.0	1192	10	BC019368	Mus muscu
C 582	11	100.0	986	6	AR509830	Sequence	C 655	11	100.0	1195	8	AY079331	Arabidops
C 583	11	100.0	986	9	HSN340461	Homo sapi	C 656	11	100.0	1196	3	CEL487543	Caenorhab
C 584	11	100.0	987	6	AR123360	Sequence	C 657	11	100.0	1207	6	AR004337	Sequence
C 585	11	100.0	987	6	I44706	Sequence 12	C 658	11	100.0	1207	6	AR004338	Sequence
C 586	11	100.0	987	6	I52112	Sequence 12	C 659	11	100.0	1207	6	AR006828	Sequence
C 587	11	100.0	987	6	AR364047	Sequence	C 660	11	100.0	1207	6	AR006829	Sequence
C 588	11	100.0	1001	6	AX081566	Sequence	C 661	11	100.0	1218	4	AF548433	Tachyglor
C 589	11	100.0	1001	6	AX374747	Sequence	C 662	11	100.0	1219	6	AR194503	Sequence
C 590	11	100.0	1002	6	AX003310	Sequence	C 663	11	100.0	1219	6	AR221954	Sequence
C 591	11	100.0	1002	6	AX003311	Sequence	C 664	11	100.0	1219	6	BD082634	Methods a
C 592	11	100.0	1012	8	AK070231	Oryza sat	C 665	11	100.0	1219	6	BD082649	Methods a
C 593	11	100.0	1015	9	BC071939	Homo sapi	C 666	11	100.0	1219	6	BD092928	Methods a
C 594	11	100.0	1022	6	AX597891	Sequence	C 667	11	100.0	1227	8	AY089181	Arabidops
C 595	11	100.0	1023	10	RNU77633	Rattus norv	C 668	11	100.0	1236	8	AF209109	Gnetum ul
C 596	11	100.0	1028	6	AR364046	Sequence	C 669	11	100.0	1244	6	AR123372	Sequence
C 597	11	100.0	1029	6	I44703	Sequence 6	C 670	11	100.0	1245	6	AR003853	Sequence
C 598	11	100.0	1029	6	I52109	Sequence 6	C 671	11	100.0	1246	8	D89206	Schizosacch
C 599	11	100.0	1037	3	AY321151	Aiptasia	C 672	11	100.0	1248	6	AR550904	Sequence
C 600	11	100.0	1039	8	MZERIP2A	Sequence	C 673	11	100.0	1248	8	AR550904	Sequence
C 601	11	100.0	1049	6	CQ716726	Sequence	C 674	11	100.0	1254	8	AF197617	Fraxaria
C 602	11	100.0	1049	9	AB036693	Homo sapi	C 675	11	100.0	1263	5	BR931396	Gallus ga
C 603	11	100.0	1053	6	AR123366	Sequence	C 676	11	100.0	1263	6	AR378743	Sequence

677	11	100.0	1263	9	AK000397	AK000397 Homo sapi	750	11	100.0	1431	6	AR319274	AR319274 Sequence
678	11	100.0	1275	6	AX654279	AX654279 Sequence	c 721	11	100.0	1431	8	BT012031	BT012031 Arabidops
679	11	100.0	1279	14	AX746606	AX746606 Hepatitis	c 752	11	100.0	1437	8	BT000184	BT000184 Arabidops
680	11	100.0	1279	14	AX746645	AX746645 Hepatitis	753	11	100.0	1443	6	AX534820	AX534820 Sequence
681	11	100.0	1280	14	AX746598	AX746598 Hepatitis	754	11	100.0	1443	6	AX534857	AX534857 Sequence
682	11	100.0	1280	14	AX746600	AX746600 Hepatitis	c 755	11	100.0	1457	5	CR387834	CR387834 Gallus ga
683	11	100.0	1280	14	AX746601	AX746601 Hepatitis	c 756	11	100.0	1470	8	AK110827	AK110827 Oryza sat
684	11	100.0	1280	14	AX746602	AX746602 Hepatitis	c 757	11	100.0	1478	3	AB017190	AB017190 Caenorhab
685	11	100.0	1280	14	AX746603	AX746603 Hepatitis	758	11	100.0	1482	3	AY163313	AY163313 Artemia f
686	11	100.0	1280	14	AX746604	AX746604 Hepatitis	759	11	100.0	1487	5	AF070478	AF070478 Gallus ga
687	11	100.0	1280	14	AX746605	AX746605 Hepatitis	760	11	100.0	1504	5	CR848559	CR848559 Xenopus t
688	11	100.0	1280	14	AX746607	AX746607 Hepatitis	761	11	100.0	1510	9	AF306347	AF306347 Homo sapi
689	11	100.0	1280	14	AX746608	AX746608 Hepatitis	762	11	100.0	1528	6	AX003308	AX003308 Sequence
690	11	100.0	1280	14	AX746644	AX746644 Hepatitis	763	11	100.0	1528	9	HSAJ5273	HSAJ5273 Homo sapi
691	11	100.0	1280	14	AX746646	AX746646 Hepatitis	c 764	11	100.0	1533	3	CEU65429	CEU65429 Caenorhabd
692	11	100.0	1280	14	AX746647	AX746647 Hepatitis	c 765	11	100.0	1536	8	AF515696	AF515696 Arabidops
693	11	100.0	1280	14	AX746648	AX746648 Hepatitis	c 766	11	100.0	1537	8	AY084766	AY084766 Arabidops
694	11	100.0	1280	14	AX746649	AX746649 Hepatitis	767	11	100.0	1538	1	AY605169	AY605169 Unculture
695	11	100.0	1280	14	AX746650	AX746650 Hepatitis	768	11	100.0	1539	5	BC075492	BC075492 Xenopus t
696	11	100.0	1280	14	AX746651	AX746651 Hepatitis	c 769	11	100.0	1543	3	HAU41810	HAU41810 Homarus ame
697	11	100.0	1280	14	AX746652	AX746652 Hepatitis	c 770	11	100.0	1543	8	AK059421	AK059421 Oryza sat
698	11	100.0	1280	14	AX746653	AX746653 Hepatitis	c 771	11	100.0	1547	6	AR506413	AR506413 Sequence
699	11	100.0	1280	14	AX746654	AX746654 Hepatitis	c 772	11	100.0	1550	5	XLU42207	XLU42207 Xenopus lae
700	11	100.0	1280	14	AX746655	AX746655 Hepatitis	c 773	11	100.0	1551	6	AX149388	AX149388 Sequence
701	11	100.0	1280	14	AX746656	AX746656 Hepatitis	c 774	11	100.0	1553	6	AX149388	AX149388 Sequence
702	11	100.0	1280	14	AX746786	AX746786 Hepatitis	c 775	11	100.0	1553	6	CO721703	CO721703 Sequence
703	11	100.0	1280	14	AX746787	AX746787 Hepatitis	c 776	11	100.0	1553	6	AX101249	AX101249 Oryza sat
704	11	100.0	1280	14	AX746788	AX746788 Hepatitis	c 777	11	100.0	1559	8	AY136384	AY136384 Arabidops
705	11	100.0	1280	14	AX746789	AX746789 Hepatitis	c 778	11	100.0	1563	1	AF507996	AF507996 Helicobac
706	11	100.0	1280	14	AX746790	AX746790 Hepatitis	c 779	11	100.0	1565	11	BV176785	BV176785 sgmm90942
707	11	100.0	1280	14	AX746791	AX746791 Hepatitis	780	11	100.0	1569	6	CO877127	CO877127 Sequence
708	11	100.0	1280	14	AX746792	AX746792 Hepatitis	781	11	100.0	1575	8	AY084269	AY084269 Arabidops
709	11	100.0	1280	14	AX746793	AX746793 Hepatitis	c 782	11	100.0	1575	9	EC072451	EC072451 Homo sapi
710	11	100.0	1280	14	AX746794	AX746794 Hepatitis	c 783	11	100.0	1578	9	AF125188	AF125188 Homo sapi
711	11	100.0	1280	14	AX746795	AX746795 Hepatitis	784	11	100.0	1585	5	BC056088	BC056088 Xenopus l
712	11	100.0	1280	14	AX746796	AX746796 Hepatitis	785	11	100.0	1587	5	BC084529	BC084529 Xenopus t
713	11	100.0	1280	14	AX746797	AX746797 Hepatitis	786	11	100.0	1587	6	AR450032	AR450032 Sequence
c 714	11	100.0	1288	14	AX746879	AX746879 Hepatitis	c 787	11	100.0	1595	8	AK060747	AK060747 Oryza sat
715	11	100.0	1293	3	DRQARF3A	AK068563 Oryza sat	788	11	100.0	1596	14	AY725240	AY725240 Canine pa
c 716	11	100.0	1294	5	BC082878	AK25063 Drosophila	789	11	100.0	1605	3	AF184925	AF184925 Trypanoso
717	11	100.0	1296	6	CS587223	BC082878 Xenopus l	c 790	11	100.0	1605	5	AF419156	AF419156 Xenopus l
718	11	100.0	1298	8	CS587223	CQ587223 Sequence	791	11	100.0	1610	5	BC072053	BC072053 Xenopus l
c 719	11	100.0	1301	8	CAR549384	AY549384 Cicer ari	792	11	100.0	1611	6	AF451233	AF451233 Sequence
c 720	11	100.0	1306	9	D89120	D89120 Schizosacch	c 793	11	100.0	1619	1	AF508012	AF508012 Helicobac
c 721	11	100.0	1308	1	S72497	AB056343 Macaca fa	c 794	11	100.0	1621	10	AB025049	AB025049 Mus muscu
c 722	11	100.0	1323	1	SHLEG	S72497 plc-beta-he	c 795	11	100.0	1624	9	BC069821	BC069821 Homo sapi
c 723	11	100.0	1323	9	F43081S20	X61716 S.aureus hl	796	11	100.0	1626	3	DROARF3B	L25064 Drosophila
724	11	100.0	1327	8	AY142691	AF243100 Homo sapi	c 797	11	100.0	1632	1	AF507999	AF507999 Helicobac
c 725	11	100.0	1350	8	AY596979	AY142691 Arabidops	c 798	11	100.0	1648	8	AY442179	AY442179 Solanum t
c 726	11	100.0	1353	6	AR545949	AY596979 Centauriu	799	11	100.0	1655	8	AK066363	AK066363 Oryza sat
c 727	11	100.0	1355	6	BD222729	AR545949 Sequence	c 800	11	100.0	1659	5	EC045911	EC045911 Danio rer
c 728	11	100.0	1357	6	CQ498403	BD222729 Human sig	c 801	11	100.0	1665	9	CR848526	CR848526 Xenopus t
729	11	100.0	1365	8	AR222861	CQ498403 Sequence	c 802	11	100.0	1665	10	BC028906	BC028906 Mus muscu
730	11	100.0	1366	3	AY071116	AY222861 Triticum	803	11	100.0	1666	9	BC067826	BC067826 Homo sapi
c 731	11	100.0	1375	9	AF002668	AY071116 Drosophil	c 804	11	100.0	1674	9	AF167173	AF167173 Homo sapi
c 732	11	100.0	1380	3	HAU66318	AF002668 Homo sapi	c 805	11	100.0	1680	8	AY128694	AY128694 Capsicu
733	11	100.0	1380	8	BT000666	U66318 Homarus ame	c 806	11	100.0	1681	5	BC077783	BC077783 Xenopus l
734	11	100.0	1381	8	BT014049	BT000666 Arabidops	c 807	11	100.0	1682	10	AK129056	AK129056 Mus muscu
735	11	100.0	1381	8	AK105808	BT014049 Lycopersi	c 808	11	100.0	1683	6	I44709	I44709 Sequence 18
736	11	100.0	1386	10	BC028860	AK105808 Oryza sat	c 809	11	100.0	1683	6	I52115	I52115 Sequence 18
737	11	100.0	1389	6	AR449841	BC028860 Mus muscu	810	11	100.0	1688	8	AF254124	AF254124 Medicago
738	11	100.0	1390	6	AX003331	AR449841 Sequence	c 811	11	100.0	1693	8	NPCAT1MR	NPCAT1MR Sequence
c 739	11	100.0	1398	6	AR354544	AX003331 Sequence	c 812	11	100.0	1695	6	I44711	I44711 Sequence 22
c 740	11	100.0	1398	6	AR353610	AR354544 Sequence	c 813	11	100.0	1695	6	I52117	I52117 Sequence 22
741	11	100.0	1408	9	BC027171	AR353610 Sequence	c 814	11	100.0	1697	5	BC066533	BC066533 Danio rer
742	11	100.0	1409	9	HSWUCRY5	BC027171 Homo sapi	c 815	11	100.0	1698	6	AX835031	AX835031 Sequence
743	11	100.0	1410	6	CQ715052	AF039396 Homo sapi	c 816	11	100.0	1702	5	BC084008	BC084008 Xenopus l
744	11	100.0	1411	8	AY341888	CQ715052 Sequence	c 817	11	100.0	1707	4	BOVSMGDS	BOVSMGDS Bovine smg
c 745	11	100.0	1414	9	AF131847	AY341888 Arabidops	818	11	100.0	1707	6	E03849	E03849 cDNA encodi
746	11	100.0	1414	10	MWKN17	AF131847 Homo sapi	c 819	11	100.0	1711	10	AF319620	AF319620 Mus muscu
c 747	11	100.0	1422	6	I44708	I44708 Mouse KIN17	c 820	11	100.0	1714	10	AB042241	AB042241 Mus muscu
c 748	11	100.0	1422	6	I52114	I52114 Sequence 16	c 821	11	100.0	1721	6	AX834869	AX834869 Sequence
749	11	100.0	1424	8	AY045798	AY045798 Arabidops	822	11	100.0	1721	6	AX834869	AX834869 Sequence

823	11	100.0	1721	9	AK097553	AK097553 Homo sapi	896	11	100.0	1922	3	AB051834	AB051834 Babesia g
c 824	11	100.0	1722	6	I44712	I44712 Sequence 24	c 897	11	100.0	1922	6	BD177422	BD177422 Uses of a
c 825	11	100.0	1722	6	I52118	I52118 Sequence 24	c 898	11	100.0	1922	6	CQ731794	CQ731794 Sequence
c 826	11	100.0	1723	9	BC008217	BC008217 Homo sapi	c 899	11	100.0	1934	6	I25465	I25465 Sequence 1
c 827	11	100.0	1725	8	AF112368	AF112368 Homo sapi	c 900	11	100.0	1937	10	MUSDRIM2	DI3545 Mus musculus
c 828	11	100.0	1732	9	AF466375	AF466375 Homo sapi	c 901	11	100.0	1939	1	AY726662	AY726662 Moraxella
c 829	11	100.0	1732	10	BC003894	BC003894 Mus muscu	c 902	11	100.0	1939	1	AY726663	AY726663 Moraxella
830	11	100.0	1734	12	AY545951	AY545951 Synthetic	c 903	11	100.0	1943	6	CQ414329	CQ414329 Sequence
831	11	100.0	1734	12	AY545952	AY545952 Synthetic	c 904	11	100.0	1944	3	AY452683	AY452683 Echinomet
832	11	100.0	1734	12	AY545953	AY545953 Synthetic	c 905	11	100.0	1946	6	CQ574101	CQ574101 Sequence
833	11	100.0	1734	12	AY545954	AY545954 Synthetic	c 906	11	100.0	1950	6	AX534800	AX534800 Sequence
834	11	100.0	1734	12	AY545955	AY545955 Synthetic	c 907	11	100.0	1951	1	HIU15056	HIU15056 Haemophilus
835	11	100.0	1734	12	AY545956	AY545956 Synthetic	c 908	11	100.0	1951	6	AR096745	AR096745 Sequence
c 836	11	100.0	1742	10	BC083118	BC083118 Mus muscu	c 909	11	100.0	1951	6	I80002	I80002 Sequence 11
c 837	11	100.0	1744	8	AF006067	AF006067 Nicotiana	c 910	11	100.0	1951	6	AR201183	AR201183 Sequence
838	11	100.0	1752	6	AX506879	AX506879 Sequence	c 911	11	100.0	1951	6	AR201643	AR201643 Sequence
c 839	11	100.0	1752	6	AX618372	AX618372 Sequence	c 912	11	100.0	1955	1	HIU15057	HIU15057 Haemophilus
c 840	11	100.0	1756	8	NTU93244	U93244 Nicotiana t	c 913	11	100.0	1955	6	AR096746	AR096746 Sequence
c 841	11	100.0	1762	6	CQ722361	CQ722361 Sequence	c 914	11	100.0	1955	6	I80003	I80003 Sequence 11
c 842	11	100.0	1764	5	AF332683	AF332683 Podarcis	c 915	11	100.0	1955	6	AR201184	AR201184 Sequence
c 843	11	100.0	1765	3	AF057743	AF057743 Thalassia	c 916	11	100.0	1955	6	AR201644	AR201644 Sequence
844	11	100.0	1766	8	AY234854	AY234854 Arabidops	c 917	11	100.0	1959	8	AY532640	AY532640 Saccharom
c 845	11	100.0	1766	9	AF100615	AF100615 Homo sapi	c 918	11	100.0	1961	10	BC075653	BC075653 Mus muscu
c 846	11	100.0	1767	10	AK129038	AK129038 Mus muscu	c 919	11	100.0	1964	10	BC019500	BC019500 Mus muscu
847	11	100.0	1769	10	MMCC7EP	Z31555 M.musculus	c 920	11	100.0	1966	5	BC082394	BC082394 Xenopus l
c 848	11	100.0	1773	9	BC002936	BC002936 Homo sapi	c 921	11	100.0	1972	3	AY113641	AY113641 Drosophil
c 849	11	100.0	1773	9	BC022845	BC022845 Homo sapi	c 922	11	100.0	1974	6	AR096744	AR096744 Sequence
850	11	100.0	1777	5	BC077572	BC077572 Xenopus l	c 923	11	100.0	1974	6	I80001	I80001 Sequence 11
851	11	100.0	1777	8	AF279780	AF279780 Homo sapi	c 924	11	100.0	1974	6	AR201182	AR201182 Sequence
c 852	11	100.0	1780	8	YSCSETHR	M85194 Saccharomyc	c 925	11	100.0	1974	6	BC020162	BC020162 Sequence
c 853	11	100.0	1784	5	BC083959	BC083959 Xenopus l	c 926	11	100.0	1974	9	BC040240	BC040240 Homo sapi
c 854	11	100.0	1787	10	BC078910	BC078910 Rattus no	c 927	11	100.0	1977	1	HIU15055	HIU15055 Haemophilus
855	11	100.0	1791	6	AX432661	AX432661 Sequence	c 928	11	100.0	1978	6	AR003582	AR003582 Sequence
c 856	11	100.0	1794	8	BT012965	BT012965 Lycopersi	c 929	11	100.0	1978	10	MMU11859	U11859 Mus musculu
c 857	11	100.0	1796	9	AK098485	AK098485 Homo sapi	c 930	11	100.0	1993	1	HIU15054	HIU15054 Haemophilus
c 858	11	100.0	1799	6	AX5919	AX5919 Sequence 58	c 931	11	100.0	1993	6	AR096743	AR096743 Sequence
859	11	100.0	1799	6	AK160372	AK160372 Sequence	c 932	11	100.0	1993	6	I80000	I80000 Sequence 10
c 860	11	100.0	1810	6	CQ843149	CQ843149 Sequence	c 933	11	100.0	1993	6	AR201181	AR201181 Sequence
c 861	11	100.0	1810	9	AF218011	AF218011 Homo sapi	c 934	11	100.0	1993	6	AR201641	AR201641 Sequence
c 862	11	100.0	1811	8	AK126115	AK126115 Homo sapi	c 935	11	100.0	1998	10	MMU17253	U17253 Mus musculu
c 863	11	100.0	1811	8	AY085828	AY085828 Arabidops	c 936	11	100.0	1998	10	MUSFI203	L14559 Mus musculu
c 864	11	100.0	1819	9	AF220185	AF220185 Homo sapi	c 937	11	100.0	2000	6	AX509709	AX509709 Sequence
c 865	11	100.0	1821	9	AF167174	AF167174 Homo sapi	c 938	11	100.0	2000	6	AX654910	AX654910 Sequence
c 866	11	100.0	1825	6	CQ604851	CQ604851 Sequence	c 939	11	100.0	2000	6	AX655332	AX655332 Sequence
c 867	11	100.0	1825	6	AR056012	AR056012 Homo sapi	c 940	11	100.0	2000	6	AX655332	AX655332 Sequence
c 868	11	100.0	1826	6	AR274916	AR274916 Homo sapi	c 941	11	100.0	2000	6	AX655332	AX655332 Sequence
c 869	11	100.0	1826	9	AF100820	AF100820 Homo sapi	c 942	11	100.0	2000	6	AX656593	AX656593 Sequence
c 870	11	100.0	1826	9	HUMORF16	DI4812 Homo sapien	c 943	11	100.0	2007	6	CQ580266	CQ580266 Sequence
c 871	11	100.0	1828	6	CQ716201	CQ716201 Sequence	c 944	11	100.0	2008	9	AF100617	AF100617 Homo sapi
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c 873	11	100.0	1831	9	BC056899	BC056899 Homo sapi	c 946	11	100.0	2009	11	BV177850	BV177850 sqm97150
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c 876	11	100.0	1844	8	AY065220	AY065220 Arabidops	c 949	11	100.0	2016	5	CAU08016	U08016 Carassius a
c 877	11	100.0	1846	10	BC083606	BC083606 Rattus no	c 950	11	100.0	2020	8	AB051137	AB051137 Macaca fa
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c 879	11	100.0	1851	6	CQ585369	CQ585369 Sequence	c 952	11	100.0	2027	8	AX335293	AX335293 Gallus ga
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c 881	11	100.0	1864	9	HSN801629	AL136859 Homo sapi	c 954	11	100.0	2052	9	BC017480	BC017480 Homo sapi
c 882	11	100.0	1878	9	BC002758	BC002758 Homo sapi	c 955	11	100.0	2055	9	BC012978	BC012978 Homo sapi
c 883	11	100.0	1879	3	AF204777	AF204777 Drosophil	c 956	11	100.0	2058	6	CQ769621	CQ769621 Sequence
c 884	11	100.0	1879	6	CQ600993	CQ600993 Sequence	c 957	11	100.0	2058	9	BC000961	BC000961 Homo sapi
c 885	11	100.0	1879	6	AX149386	AX149386 Sequence	c 958	11	100.0	2060	9	BC012978	BC012978 Homo sapi
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c 893	11	100.0	1914	5	BC045876	BC045876 Danilo rer	c 966	11	100.0	2104	9	AK054621	AK054621 Homo sapi
c 894	11	100.0	1914	9	AB038155	AB038155 Homo sapi	c 967	11	100.0	2107	3	AY305522	AY305522 Skogseberg
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Db 11 CTTGGCACTA 1

RESULT 3			
AX201811			
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DEFINITION	Sequence 20 from Patent WO0153537.		linear
			PAT 30-AUG-2001

KEYWORDS	ORGANISM
SOURCE	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	1
AUTHORS	Moskowitz, D.W.
TITLE	Nitric oxide synthase gene diagnostic polymorphisms
JOURNAL	Patent: WO 0153537-A 20 26-JUL-2001;
FEATURES	Dzgenes, L.I.C. (US) Location/Qualifiers

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/mcl_type="unassigned DNA"
/db_xref="taxon:9606"
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Db  
1 CTTGGCACTA 11

RESUBMIT #	LOCUS	AX003312	22 bp	DNA	linear	PAT 24-AUG-2000
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		DEFINITION	Sequence 5 from Patent WO9929845.			

VERSION  
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 KEYWORDS  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens

DEFINITION	SEQUENCE 20 FROM PATENT WO0153537.
ACCESSION	AX201811

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Angulo-Mora,J.F. and Mauffrey,P.
TITLE Sequences coding for kin17 protein and their applications
JOURNAL Patent: WO 9329845-A 5 17-JUN-1999;
ANGULO MORA JAIME FRANCISCO (FR); COMMISSARIAT ENERGIE ATOMIQUE
(FR)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.4e+03;
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RESULT 5
BD095189/c
LOCUS
DEFINITION Novel polypeptide, novel DNA, novel antibody, and novel genetic
modified animal.
ACCESSION BD095189
VERSION BD095189.1 GI:22640777
KEYWORDS WO 0138529-A/7.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1 (bases 1 to 23)
REFERENCE Shiraishi,N., Sekine,S., Nabeshima,Y., Fujimori,T. and Ito,S.
AUTHORS Novel polypeptide, novel DNA, novel antibody, and novel genetic
TITLE modified animal
JOURNAL Patent: WO 0138529-A 7 31-MAY-2001;
KYOWA HAKKO KOGYO CO LTD,NORIHIKO SHIRAISHI,SUSUMU SEKINE,YOICHI
NABESHIMA,TOSHIHIKO FUJIMORI,SHINJI ITO
COMMENT PN WO 0138529-A/7
PD 31-MAY-2001
PF 17-NOV-2000 WO 2000JP008121
PR 19-NOV-1999 JP 99P 329649
PI NORIHIKO SHIRAISHI,SUSUMU SEKINE,YOICHI NABESHIMA,TOSHIHIKO
PI FUJIMORI,
PI SHINJI ITO
PC C12N15/12,C07K14/47,C07K16/18,A61K38/17,A61P43/00,G01N33/53,
PC C12N15/85,
PC C12N1/21,C12P21/02,C12Q1/68,A01K67/027,C12Q1/02 CC
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Location/Qualifiers
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FT /organism='Artificial Sequence'.
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source Location/Qualifiers
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Db 13 CTTTGGCACTA 3
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RESULT 6
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LOCUS
DEFINITION Sequence 7 from Patent WO0233106.
ACCESSION AX427666
VERSION AX427666.1 GI:21537785
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
AUTHORS Plant cell death system
TITLE Patent: WO 0233106-A 7 25-APR-2002;
JOURNAL CAMBRIDGE ADVANCED TECH (GB)
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source Location/Qualifiers
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/notes="Introduced restriction sites"
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Db 40 CTTTGGCACTA 30
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RESULT 7
CQ057099
LOCUS
DEFINITION Sequence 7919 from Patent WO0157270.
ACCESSION CQ057099
VERSION CQ057099.1 GI:41031605
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human breast and hbl 100 cells
JOURNAL Patent: WO 0157270-A 7919 09-AUG-2001;
Aecomica, Inc. (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
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RESULT 8
CQ076362
LOCUS

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DEFINITION Sequence 12162 from Patent WO0157278.
ACCESSION CQ076362
VERSION CQ076362.1 GI:41046231
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human hela cells or other human
cervical epithelialcells
JOURNAL Patent: WO 0157278-A 12162 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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AL163247.2, EVALUE 4.00e-11"
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Query Match 100.0%; Score 11; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
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Db 34 CTTTGGCACTA 44

RESULT 9
CQ107351
LOCUS
DEFINITION Sequence 16210 from Patent WO0157272.
ACCESSION CQ107351
VERSION CQ107351.1 GI:41076404
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 16210 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Qy 1 CTTTGGCACTA 11
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RESULT 10
CQ146017
LOCUS
DEFINITION Sequence 16062 from Patent WO0157273.
ACCESSION CQ146017
VERSION CQ146017.1 GI:41153367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 16039 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Db 34 CTTTGGCACTA 44

RESULT 11
CQ205816
LOCUS
DEFINITION Sequence 8093 from Patent WO0157271.
ACCESSION CQ205816
VERSION CQ205816.1 GI:41191920
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and Dt 474 cells
JOURNAL Patent: WO 0157271-A 8093 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Db 34 CTTTGGCACTA 44

RESULT 12
CQ229223
LOCUS
DEFINITION Sequence 16062 from Patent WO0157273.
ACCESSION CQ229223
VERSION CQ229223
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and Dt 474 cells
JOURNAL Patent: WO 0157271-A 8093 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Qy 1 CTTTGGCACTA 11
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Db 34 CTTTGGCACTA 44
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ACCESSION      CQ229223
VERSION        CQ229223.1  GI:41212441
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE         HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
               ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
               60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
               August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
               (03.10.00)<150> US 60/236,359<151> 27 September 2000
               (27.09.00)<150> US 60/234,687<151> 21 September 2000
               (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
               Molecular Dynamics Sequence Listing Engine
JOURNAL        Patent: WO 0157273-A 16062 09-AUG-2001;
               Aeomica, Inc. (US)
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Query Match      100.0%; Score 11; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
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Db      34 CTTTGGCACTA 44

RESULT 13
LOCUS      CQ267352
DEFINITION Sequence 15613 from Patent WO0157277.
ACCESSION  CQ267352
VERSION    CQ267352.1  GI:41239956
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
               analysis of gene expression in human fetal liver
JOURNAL     Patent: WO 0157277-A 15613 09-AUG-2001;
               Aeomica, Inc. (US)
FEATURES    1..77
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
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Db      34 CTTTGGCACTA 44

ACCESSION      CQ229223
VERSION        CQ229223.1  GI:41212441
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE         HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
               ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
               60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
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               (27.09.00)<150> US 60/234,687<151> 21 September 2000
               (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
               Molecular Dynamics Sequence Listing Engine
JOURNAL        Patent: WO 0157273-A 16062 09-AUG-2001;
               Aeomica, Inc. (US)
FEATURES       1..77
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
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Db      34 CTTTGGCACTA 44

RESULT 15
LOCUS      CQ341641
DEFINITION Sequence 15735 from Patent WO0157275.
ACCESSION  CQ341641
VERSION    CQ341641.1  GI:41290712
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
               analysis of gene expression in human brain
JOURNAL     Patent: WO 0157275-A 15735 09-AUG-2001;
               Aeomica, Inc. (US)
FEATURES    1..77
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Query Match      100.0%; Score 11; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
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Db      34 CTTTGGCACTA 44
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RESULT 14
LOCUS      CQ304373
DEFINITION Sequence 15478 from Patent WO0186003.
ACCESSION  CQ304373
VERSION    CQ304373.1  GI:41264950
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
               analysis of gene expression in human lung
JOURNAL     Patent: WO 0186003-A 15478 15-NOV-2001;
               Aeomica, Inc. (US)
FEATURES    1..77
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
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Db      34 CTTTGGCACTA 44
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RESULT 15
LOCUS      CQ341641
DEFINITION Sequence 15735 from Patent WO0157275.
ACCESSION  CQ341641
VERSION    CQ341641.1  GI:41290712
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
               analysis of gene expression in human brain
JOURNAL     Patent: WO 0157275-A 15735 09-AUG-2001;
               Aeomica, Inc. (US)
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ORIGIN
Query Match      100.0%; Score 11; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
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Db      34 CTTTGGCACTA 44
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RESULT 15
LOCUS      CQ341641
DEFINITION Sequence 15735 from Patent WO0157275.
ACCESSION  CQ341641
VERSION    CQ341641.1  GI:41290712
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
               analysis of gene expression in human brain
JOURNAL     Patent: WO 0157275-A 15735 09-AUG-2001;
               Aeomica, Inc. (US)
FEATURES    1..77
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Query Match      100.0%; Score 11; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
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Db      34 CTTTGGCACTA 44
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RESULT 16  
AX910296  
LOCUS AX910296 100 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 26159 from Patent EP1033401.  
ACCESSION AX910296  
VERSION AX910296.1 GI:40066376  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.  
AUTHORS Expressed sequence tags and encoded human proteins  
TITLE Patent: EP 1033401-A 26159 06-SEP-2000;  
JOURNAL Genset (FR)  
FEATURES  
source Location/Qualifiers  
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Db 81 CTTTGGCACTA 91  
RESULT 17  
BD045829  
LOCUS BD045829 100 bp DNA linear PAT 27-AUG-2002  
DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD045829  
VERSION BD045829.1 GI:22587571  
KEYWORDS JP 2001269182-A/22075.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 100)  
REFERENCE Edwards, J.B.D.M., Duclair, B. and Jordan, J.Y.  
AUTHORS Sequence tag and encoded human protein  
TITLE Patent: JP 2001269182-A 22075 02-OCT-2001;  
JOURNAL GENSET  
COMMENT QS Homo sapiens (human)  
PN JP 2001269182-A/22075  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES  
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC  
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Qy 1 CTTTGGCACTA 11  
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Db 81 CTTTGGCACTA 91  
RESULT 18  
AX325267  
LOCUS AX325267 121 bp DNA linear PAT 02-SEP-2002  
DEFINITION Sequence 1405 from Patent WO0192512.  
ACCESSION AX325267  
VERSION AX325267.1 GI:18096023  
KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1  
REFERENCE Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
AUTHORS Targeted chromosomal genomic alterations in plants using modified  
TITLE single stranded oligonucleotides  
JOURNAL Patent: WO 0192512-A 1405 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
FEATURES  
source Location/Qualifiers  
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Qy 1 CTTTGGCACTA 11  
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Db 23 CTTTGGCACTA 33  
RESULT 19  
AX325268  
LOCUS AX325268 121 bp DNA linear PAT 02-SEP-2002  
DEFINITION Sequence 1406 from Patent WO0192512.  
ACCESSION AX325268  
VERSION AX325268.1 GI:18096024  
KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1  
REFERENCE Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
AUTHORS Targeted chromosomal genomic alterations in plants using modified  
TITLE single stranded oligonucleotides  
JOURNAL Patent: WO 0192512-A 1406 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
FEATURES  
source Location/Qualifiers  
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Query Match 100.0%; Score 11; DB 6; Length 121;  
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Matches 11; Conservative 0;  
Qy 1 CTTTGGCACTA 11  
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Db 99 CTTTGGCACTA 89



RESULT 20  
G00343  
LOCUS  
DEFINITION  
129 bp DNA linear STS 28-SEP-1998  
SWS5785 Eric D. Green Homo sapiens STS genomic, sequence tagged  
site.  
ACCESSION  
G00343  
VERSION  
G00343.1 GI:485201  
SOURCE  
STS.  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 129)  
Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F.,  
Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.,  
Leckie,M.P. and Green,E.D.  
A collection of 1814 human chromosome 7-specific STSs  
Genome Res. 7 (1), 59-64 (1997)  
97189344  
9037602  
PUBMED  
1 (bases 1 to 129)  
Green,E.D.  
Human chromosome 7 STSs (1997)  
Unpublished (1997)  
COMMENT  
GDB: GDB:1317228  
Contact: Eric D. Green  
Genome Technology Branch  
National Human Genome Research Institute/NIH  
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892  
Tel: 3014020201  
Fax: 3014024735  
Email: egreen@nhgri.nih.gov  
Primer A: TGCACCTATTGCAATG  
Primer B: AGCCAGTTATGTCATAG  
STS size: 67  
PCR Profile:  
Presoak: 0 degrees C for 0.00 minute(s)  
Denaturation: 92 degrees C for 1.00 minute(s)  
Annealing: 60 degrees C for 2.00 minute(s)  
Polymerization: 72 degrees C for 2.00 minute(s)  
PCR Cycles: 35  
Thermal Cycler: PerkinElmer TC  
Protocol:  
Template: 30-100 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/ul  
Total Vol: 5 ul  
Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 8.3

The sequence for this STS was derived from a single sequencing read. For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/STB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID=92128937].

## FEATURES

source

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primer\_bind  
complement(101..118)

## ORIGIN

Query Match 100.0%; Score 11; DB 11; Length 129;

Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTGGCACTA 11  
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DB 93 CTTTGGCACTA 103  
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RESULT 21  
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LOCUS  
DEFINITION  
149 bp DNA linear STS 12-JUN-2003  
BX284306  
Arabidopsis thaliana transposon insertion STS SM\_3.23750, sequence tagged site.  
ACCESSION  
BX284306  
VERSION  
BX284306.1 GI:28803979  
KEYWORDS  
STS; STS, sequence tagged site.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE  
1  
Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,  
Murphy,G., Langham,S., Legrys,C., Jones,J.D.G. and Bevan,M.  
Unpublished

JOURNAL  
REFERENCE  
2 (bases 1 to 149)  
AUTHORS  
Clarke,J.H.

TITLE  
Direct Submission  
JOURNAL  
Submitted (03-MAR-2003) Clarke J.H., John Innes Centre, Colney

COMMENT  
Lane, Norwich, NR4 7UJ, UK  
AT denotes an activation tag dissociation transposon within a  
single line, ET an enhancer trap dissociation transposon, GT a gene  
trap dissociation transposon, MT a mis-expression enhancer trap  
dissociation transposon, SM a defective suppressor mutator  
transposon. \_3 denotes a sequence derived from the 3' end of the  
transposon, \_5 denotes a sequence derived from the 5' end of the  
transposon, BBSRC GARNET, ATIS project

On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock  
code: DEAD.  
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/db\_xref="taxon:3702"  
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/standard\_name="SM\_3.23750"

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Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
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DB 124 CTTTGGCACTA 134  
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RESULT 22  
CQ659646/c

LOCUS  
DEFINITION  
Sequence 4572 from Patent WO02070737.  
ACCESSION  
CQ659646  
VERSION  
CQ659646.1 GI:42128603  
KEYWORDS  
Homo sapiens (human)

SOURCE  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1  
Liew,C.C., Marshall,W.E. and Zhang,H.

```

TITLE      Compositions and methods relating to osteoarthritis
JOURNAL    Patent: WO 02070737-A 4572 12-SEP-2002;
           Chondrogene Inc. (CA)
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           /mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
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Db 139 CTTTGGCACTA 129

RESULT 23
CQ058212/c
LOCUS      CQ058212 153 bp DNA linear PAT 19-JAN-2004
DEFINITION Sequence 9032 from Patent WO0157270.
ACCESSION  CQ058212
VERSION    CQ058212.1 GI:41032718
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human breast and hbl 100 cells
           Patent: WO 0157270-A 9032 09-AUG-2001;
JOURNAL    Aeomica, Inc. (US)
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           3.90e+00"
ORIGIN
Query Match      100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
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Db 99 CTTTGGCACTA 89

RESULT 24
CQ077548/c
LOCUS      CQ077548 153 bp DNA linear PAT 20-JAN-2004
DEFINITION Sequence 13348 from Patent WO0157278.
ACCESSION  CQ077548
VERSION    CQ077548.1 GI:41047417
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human hela cells or other human
           cervical epithelial cells
           Patent: WO 0157278-A 13348 09-AUG-2001;
JOURNAL    Aeomica, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 8.5e+03;
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Db 99 CTTTGGCACTA 89

RESULT 25
CQ108562/c
LOCUS      CQ108562 153 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17421 from Patent WO0157272.
ACCESSION  CQ108562
VERSION    CQ108562.1 GI:41077615
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human placenta
           Patent: WO 0157272-A 17421 09-AUG-2001;
JOURNAL    Aeomica, Inc. (US)
FEATURES   source
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           3.90e+00"
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Query Match      100.0%; Score 11; DB 6; Length 153;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 99 CTTTGGCACTA 89

RESULT 26
CQ147196/c
LOCUS      CQ147196 153 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17218 from Patent WO0157276.
ACCESSION  CQ147196
VERSION    CQ147196.1 GI:41154546
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human bone marrow
           Patent: WO 0157276-A 17218 09-AUG-2001;
JOURNAL    Aeomica, Inc. (US)
FEATURES   source
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Query Match      100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 99 CTTTGGCACTA 89

RESULT 27
CQ147196/c
LOCUS      CQ147196 153 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17218 from Patent WO0157276.
ACCESSION  CQ147196
VERSION    CQ147196.1 GI:41154546
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE     Human genome-derived single exon nucleic acid probes useful for
           analysis of gene expression in human bone marrow
           Patent: WO 0157276-A 17218 09-AUG-2001;
JOURNAL    Aeomica, Inc. (US)
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Query Match      100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 99 CTTTGGCACTA 89
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JOURNAL Patent: WO 0157276-A 17218 09-AUG-2001;  
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AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE  
3.90e+00"

ORIGIN  
Query Match 100.0%; Score 11; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 99 CTTTGGCACTA 89

RESULT 27  
CQ182574/c  
LOCUS 153 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 13970 from Patent WO0157274.  
ACCESSION CQ182574  
VERSION CQ182574.1 GI:41177360  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human heart  
TITLE Patent: WO 0157274-A 13970 09-AUG-2001;  
JOURNAL Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1..153  
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/note="MAP TO AL035633.15-EXPRESSED IN HEART, SIGNAL =  
2.1-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT:  
AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE  
3.90e+00"

ORIGIN  
Query Match 100.0%; Score 11; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 99 CTTTGGCACTA 89

RESULT 28  
CQ206983/c  
LOCUS 153 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 9260 from Patent WO0157271.  
ACCESSION CQ206983  
VERSION CQ206983.1 GI:41193087  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human liver  
TITLE Patent: WO 0157271-A 9260 09-AUG-2001;  
JOURNAL Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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= 1.8-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT:  
AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE  
3.90e+00"

ORIGIN  
Query Match 100.0%; Score 11; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 99 CTTTGGCACTA 89

RESULT 29  
CQ230434/c  
LOCUS 153 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 17273 from Patent WO0157273.  
ACCESSION CQ230434  
VERSION CQ230434.1 GI:41213652  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO  
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US  
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03  
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000  
(03.10.00)<150> US 60/236,359<151> 27 September 2000  
(27.09.00)<150> US 60/234,687<151> 21 September 2000  
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>  
Molecular Dynamics Sequence Listing Engine  
TITLE Patent: WO 0157273-A 17273 09-AUG-2001;  
JOURNAL Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
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1..153  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE  
3.90e+00"

ORIGIN  
Query Match 100.0%; Score 11; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||||  
Db 99 CTTTGGCACTA 89

RESULT 30  
CQ268567/c  
LOCUS 153 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 16928 from Patent WO0157277.  
ACCESSION CQ268567  
VERSION CQ268567.1 GI:41241171

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver  
JOURNAL Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver  
PATENT: WO 0157277-A 16828 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/note="MAP TO AL035633.15-EXPRESSED IN FETAL LIVER, SIGNAL = 2.4-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT: AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE 3.90e+00"

ORIGIN  
Query Match 100.0%; Score 11; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
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Db 99 CTTTGGCACTA 89

RESULT 31  
CQ305599/c  
LOCUS CQ305599 153 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 16704 from Patent WO0186003.  
ACCESSION CQ305599  
VERSION CQ305599.1 GI:41266176  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung  
JOURNAL Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung  
PATENT: WO 0186003-A 16704 15-NOV-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/note="MAP TO AL035633.15-EXPRESSED IN LUNG, SIGNAL = 2.6-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT: AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE 3.90e+00"

ORIGIN  
Query Match 100.0%; Score 11; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 99 CTTTGGCACTA 89

RESULT 32  
CQ342787/c  
LOCUS CQ342787 153 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 16881 from Patent WO0157275.  
ACCESSION CQ342787

CQ342787.1 GI:41291858  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain  
JOURNAL Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain  
PATENT: WO 0157275-A 16881 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. .153  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AL035633.15-EXPRESSED IN BRAIN, SIGNAL = 2.3-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT: AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE 3.90e+00"

ORIGIN  
Query Match 100.0%; Score 11; DB 6; Length 153;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 99 CTTTGGCACTA 89

RESULT 33  
ATH553769  
LOCUS ATH553769 198 bp DNA linear PLN 29-MAR-2003  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 368C09.  
ACCESSION AJ553769  
VERSION AJ553769.1 GI:29370234  
KEYWORDS left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
REFERENCE  
AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565  
REFERENCE 2 (bases 1 to 198)  
AUTHORS Balzergue, S.  
TITLE Direct Submission  
JOURNAL Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr/>).

FEATURES  
source Location/Qualifiers  
1. .198  
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/db\_xref="taxon:3702"  
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/clone.lib="Arabidopsis thaliana T-DNA insertion lines"  
1..198  
note="T-DNA flanking sequence  
left border"

misc\_feature

ORIGIN

Query Match 100.0%; Score 11; DB 8; Length 198;  
Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
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Db 33 CTTTGGCACTA 43

RESULT 34  
BV201964  
LOCUS BV201964 201 bp DNA linear STS 10-JUN-2004  
DEFINITION sqm207837 Human DNA (Sequenom) Homo sapiens STS genomic, sequence tagged site.  
ACCESSION BV201964  
VERSION BV201964.1 GI:48170922  
KEYWORDS STS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 201)  
AUTHORS Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.  
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions  
JOURNAL  
COMMENT Genome Res. (2004) In press  
Contact: Andreas Braun  
Pharmaceuticals division  
Sequenom, Inc.  
3595 John Hopkins Court, San Diego, CA 92121, USA  
Tel: 18582029018  
Fax: 18582029020  
Email: abraun@sequenom.com  
Primer A: No primer sequence submitted  
Primer B: No primer sequence submitted  
STS size: 201.

FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone.lib="Human DNA (Sequenom)"  
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STS

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 9 CTTTGGCACTA 19

RESULT 35  
AX618370/c  
LOCUS AX618370 204 bp DNA linear PAT 20-FEB-2003  
DEFINITION Sequence 1333 from Patent WO2094868.  
ACCESSION AX618370  
VERSION AX618370.1 GI:28448504  
KEYWORDS

SOURCE Staphylococcus aureus  
ORGANISM Staphylococcus aureus  
Bacteria; Firmicutes; Bacillales; Staphylococcus.  
REFERENCE 1  
AUTHORS Maignani,V.C., Mora,M.C. and Scarselli,M.C.  
TITLE Staphylococcus aureus proteins and nucleic acids  
JOURNAL Patent: WO 02094868-A 1333 28-NOV-2002;  
Chiron Spa (IT)  
FEATURES  
Location/Qualifiers  
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/organism="Staphylococcus aureus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:1280"

ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 204;  
Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 109 CTTTGGCACTA 99

RESULT 36  
AR553184/c  
LOCUS AR553184 207 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 8315 from patent US 6747137.  
ACCESSION AR553184  
VERSION AR553184.1 GI:53946359  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 207)  
AUTHORS Weinscock,K.G. and Bush,D.  
TITLE Nucleic acid sequences relating to Candida albicans for diagnostics and therapeutics  
JOURNAL Patent: US 6747137-A 8315 08-JUN-2004;  
FEATURES  
Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 207;  
Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 178 CTTTGGCACTA 168

RESULT 37  
ATH526781/c  
LOCUS ATH526781 226 bp DNA linear PLN 29-MAR-2003  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 126D03.  
ACCESSION AJ526781  
VERSION AJ526781.1 GI:26795041  
KEYWORDS left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
REFERENCE 1  
AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelleier,G., Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
 MEDLINE 22363535  
 PUBMED 12446565  
 REFERENCE 2 (bases 1 to 226)  
 AUTHORS Balzerque, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Versailles). The DNA fragment (g) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
 source  
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 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 misc\_feature  
 1..226  
 /note="T-DNA flanking sequence left border"

ORIGIN  
 Query Match 100.0%; Score 11; DB 8; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 57 CTTTGGCACTA 47

RESULT 38  
 BV084044 232 bp DNA linear STS 30-SEP-2003  
 LOCUS sc1275\_p3 Ky21 Zea mays Ky21 Zea mays STS genomic, sequence tagged  
 DEFINITION site.  
 ACCESSION BV084044  
 VERSION BV084044.1 GI:37055701  
 KEYWORDS STS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 232)  
 AUTHORS McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.  
 TITLE MPZ-UCI Joint SNP Discovery  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Brandon S. Gaut  
 Dept. Ecology and Evolutionary Biology  
 U.C. Irvine  
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA  
 Tel: (949) 824-2564  
 Fax: (949) 824-2181  
 Email: bgaut@uci.edu  
 Primer A: ATCTACCAATGCCTCCATATTT  
 Primer B: GTTGTAGCAGTACAGCCAGTTCA  
 Protocol:  
 PCR amplification of genomic DNA  
 Template: 50 ng  
 Primer: each 0.5 uM  
 dNTPs: each 200 uM

Tag Polymerase: RedTaq (Sigma)  
 Total Vol: 10 ul  
 Amplification sequencing  
 ABI protocol - using d-Rhodamine terminator cycle  
 sequencing ready reaction with ampliTaq DNA polymerase FS  
 Sequence ran on ABI 3700 sequencer.

Buffer:  
 Genomic DNA amplification  
 RedTaq (Sigma)  
 Sequencing buffer  
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 40 56 71 71 75 80 80 69 65 63 61 53  
 57 72 71 71 61 62 61 76 82 85 90 90 78 74 74 72 61 62 59 64 64  
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FEATURES  
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 /cultivar="Ky21"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Zea mays Ky21"  
 /dev stage="seedling"  
 /note="Organ: leaf; genomic DNA from inbred line"  
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ORIGIN  
 Query Match 100.0%; Score 11; DB 11; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
 |||||  
 Db 53 CTTTGGCACTA 63

RESULT 39  
 BX467061 234 bp DNA linear STS 10-JUN-2003  
 LOCUS Arabidopsis thaliana transposon insertion STS SM\_3.38432, sequence  
 DEFINITION tagged site.  
 ACCESSION BX467061  
 VERSION BX467061.1 GI:30141627  
 KEYWORDS STS; STS, sequence tagged site.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1  
 AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Langanham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.  
 TITLE Unpublished  
 REFERENCE 2 (bases 1 to 234)  
 AUTHORS Clarke, J.H.  
 JOURNAL Direct Submission  
 COMMENT Submitted (25-APR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK  
 AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, Gr a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. \_3 denotes a sequence derived from the 3' end of the transposon. \_5 denotes a sequence derived from the 5' end of the transposon. BSRG GARNet, ARIS project  
 On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N125143.

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 /mol\_type="genomic DNA"

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/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AC007505"
/note="Derived from superpool 16.15 NASC code N40710"
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/standard_name="SM_3.38432"

STIS

ORIGIN
Query Match 100.0%; Score 11; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
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Db 84 CTTTGGCACTA 94

RESULT 40
BX467053
LOCUS
DEFINITION Arabidopsis thaliana transposon insertion STS SM_3.38431, sequence
tagged site.
ACCESSION BX467053
VERSION BX467053.1 GI:30141619
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
1 Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,
Murphy,G., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.
Unpublished
2 (bases 1 to 245)
Clarke,J.H.
Direct Submission
Submitted (25-APR-2003) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, Gr a gene
trap dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. 3 denotes a sequence derived from the 3' end of the
transposon, 5 denotes a sequence derived from the 5' end of the
transposon. BEBRC GARNET, ARIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: N125142.
Location/Qualifiers
1..245
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AC007505"
/note="Derived from superpool 16.15 NASC code N40710"
1..245
/standard_name="SM_3.38431"

STIS

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
    |||
Db 84 CTTTGGCACTA 94

RESULT 41
CQ450823/c
LOCUS
DEFINITION Sequence 16583 from Patent WO0192523.

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```

ACCESSION CQ450823
VERSION CQ450823.1 GI:41419642
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 Shimkets,R.A. and Leach,M.D.
AUTHORS Human polynucleotides and polypeptides encoded thereby
TITLE Patent: WO 0192523-A 16583 06-DEC-2001;
JOURNAL Curagen Corporation (US)
FEATURES
    Location/Qualifiers
    1..246
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 246;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
    |||
Db 24 CTTTGGCACTA 14

RESULT 42
BV084038
LOCUS
DEFINITION sc1275_p3 CML333 Zea mays CML333 Zea mays STS genomic, sequence
tagged site.
ACCESSION BV084038
VERSION BV084038.1 GI:37055695
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 250)
AUTHORS McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE MP2-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ATCCTACCAATGCCCTCATATTT
Primer B: GTTGTAGCAGTACAGCCAGTTCA
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

```

PHRED/PHRAP Quality Scores 40 60 64 58 53 54 49 49 54 53 58 64 53  
53 57 59 61 59 73 66 65 62 62 76 69 77 75 78 75 70 64 62 60 71 71  
75 75 75 56 56 56 56 39 34 34 34 34 7 7 37 37 39 58 67 64 59  
55 61 64 59 59 55 50 52 52 60 59 66 60 64 62 60 64 60 55 59  
65 72 80.

#### FEATURES

#### source

Location/Qualifiers  
1. .250  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="CML333"  
/db\_xref="taxon:4577"  
/clone\_lib="Zea mays CML333"  
/dev\_stage="seedling"  
/note="Organ: leaf; genomic DNA from inbred line"  
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#### STS

#### ORIGIN

Query Match 100.0%; Score 11; DB 11; Length 250;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 71 CTTTGGCACTA 81

#### RESULT 43

#### LOCUS

DEFINITION BV084041 250 bp DNA linear STS 30-SEP-2003  
scl275\_p3 Ill14H Zea mays Ill14H Zea mays STS genomic, sequence  
tagged site.

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

1 (bases 1 to 250)  
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.  
MPZ-UCI Joint SNP Discovery  
Unpublished (2003)

Contact: Brandon S. Gaut

Dept. Ecology and Evolutionary Biology

U.C. Irvine

321 Steinhaus Hall, Irvine, CA 92697-2525, USA

Tel: (949) 824-2564

Fax: (949) 824-2181

Email: bgaut@uci.edu

Primer A: ATCCTACCAATGCCCTCATATTT

Primer B: GTTGTAGCAGTACAGCCAGTTCA

Protocol:

PCR amplification of genomic DNA

Template: 50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Taq Polymerase: RedTaq (Sigma)

Total Vol: 10 ul

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle

sequencing ready reaction with amplitaq DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification

RedTaq (Sigma)

Sequencing buffer

d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 69 69 59 52 49 53 46 44 44 50 56 52  
52 56 58 63 60 67 58 57 57 60 53 57 54 52 58 53 56 64 66 65 73

#### FEATURES

#### source

Location/Qualifiers  
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/organism="Zea mays"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:4577"  
/clone\_lib="Zea mays Ill14H"  
/dev\_stage="seedling"  
/note="Organ: leaf; genomic DNA from inbred line"  
<1. .>250

#### STS

#### ORIGIN

Query Match 100.0%; Score 11; DB 11; Length 250;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 71 CTTTGGCACTA 81

#### RESULT 44

#### LOCUS

DEFINITION BV084045 250 bp DNA linear STS 30-SEP-2003  
scl275\_p3 M37W Zea mays M37W Zea mays STS genomic, sequence tagged  
site.

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

1 (bases 1 to 250)  
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.  
MPZ-UCI Joint SNP Discovery  
Unpublished (2003)

Contact: Brandon S. Gaut

Dept. Ecology and Evolutionary Biology

U.C. Irvine

321 Steinhaus Hall, Irvine, CA 92697-2525, USA

Tel: (949) 824-2564

Fax: (949) 824-2181

Email: bgaut@uci.edu

Primer A: ATCCTACCAATGCCCTCATATTT

Primer B: GTTGTAGCAGTACAGCCAGTTCA

Protocol:

PCR amplification of genomic DNA

Template: 50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Taq Polymerase: RedTaq (Sigma)

Total Vol: 10 ul

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle

sequencing ready reaction with amplitaq DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification

RedTaq (Sigma)

Sequencing buffer

d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 69 73 61 48 48 39 41 42 47 54 59 52  
52 34 34 26 26 26 26 45 45 51 66 66 75 76 80 69 65 60 55 60 68  
75 74 74 56 56 56 56 56 35 35 35 35 9 9 51 51 45 69 74 72 76  
69 68 63 66 68 58 55 55 55 55 71 73 74 66 73 76 55 59 55 60 60



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    67 69 76. Location/Qualifiers
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      /organism="Zea mays"
      /mol_type="genomic DNA"
      /cultivar="M37W"
      /db_xref="taxon:4577"
      /clone_lib="Zea mays M37W"
      /dev_stage="seedling"
      /note="Organ: leaf; genomic DNA from inbred line"
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    STS
    ORIGIN
      Query Match 100.0%; Score 11; DB 11; Length 250;
      Best Local Similarity 100.0%; Pred. No. 8.3e+03;
      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY 1 CTTTGGCACTA 11
      Db 71 CTTTGGCACTA 81
      RESULT 45
      LOCUS BV084046 250 bp DNA linear STS 30-SEP-2003
      DEFINITION sci275_p3 Hp301 Zea mays Hp301 Zea mays STS genomic, sequence
      tagged site.
      ACCESSION BV084046
      VERSION BV084046.1 GI:37055703
      KEYWORDS STS.
      ORGANISM Zea mays
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
      clade; Panicoideae; Andropogoneae; Zea.
      1 (bases 1 to 250)
      McMillen,M.D., Vroth Bi,I., Schroeder,S.S. and Gaut,B.S.
      MPZ-UCI Joint SNP Discovery
      Unpublished (2003)
      CONTACT: Brandon S. Gaut
      Dept. Ecology and Evolutionary Biology
      U.C. Irvine
      321 Steinhaus Hall, Irvine, CA 92697-2525, USA
      Tel: (949) 824-2564
      Fax: (949) 824-2181
      Email: bgaut@uci.edu
      Primer A: ATCCATCAATGCCCTCATATTT
      Primer B: GTTGACAGTACAGCCAGTTCA
      PCR amplification of genomic DNA
      Protocol:
      Template: 50 ng
      Primers: each 0.5 uM
      dNTPs: each 200 uM
      Taq Polymerase: RedTaq (Sigma)
      Total Vol: 10 ul
      Amplicon sequencing
      ABI protocol - using d-Rhodamine terminator cycle
      sequencing ready reaction with ampliTaq DNA polymerase FS
      Sequence ran on ABI 3700 sequencer.
      Buffer:
      Genomic DNA amplification
      RedTaq (Sigma)
      Sequencing buffer
      d-Rhodamine kit (ABI)
      PHRED/PHRAP Quality Scores 61 64 57 51 50 49 49 54 54 64 61 58 58
      40 40 40 26 26 26 51 51 56 72 71 77 76 73 76 71 66 66 73 72
      71 71 71 76 75 75 82 83 88 75 69 75 75 65 64 59 57 63 63 65 65
      65 59 70 65 64 62 59 54 54 55 54 54 66 66 68 60 60 59 55 57 55 60
      60 66 68 7.
      Location/Qualifiers
    FEATURES
      source
        67 69 76. Location/Qualifiers
          1..250
          /organism="Zea mays"
          /mol_type="genomic DNA"
          /cultivar="M37W"
          /db_xref="taxon:4577"
          /clone_lib="Zea mays M37W"
          /dev_stage="seedling"
          /note="Organ: leaf; genomic DNA from inbred line"
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        STS
        ORIGIN
          Query Match 100.0%; Score 11; DB 11; Length 250;
          Best Local Similarity 100.0%; Pred. No. 8.3e+03;
          Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
          QY 1 CTTTGGCACTA 11
          Db 71 CTTTGGCACTA 81
          RESULT 46
          LOCUS G15461 250 bp DNA linear STS 04-JAN-1996
          DEFINITION human STS SHGC-16885, sequence tagged site.
          ACCESSION G15461
          VERSION G15461.1 GI:1132224
          KEYWORDS STS; STS sequence; primer; sequence tagged site.
          SOURCE Homo sapiens
          ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 250)
          Myers,R.M.
          Unpublished (1995)
          CONTACT: Richard M. Myers
          Stanford Human Genome Center (SHGC)
          Stanford University School of Medicine
          Department of Genetics, M-344, Stanford, CA 94305, USA
          Tel: 4157259687
          Fax: 4157259689
          Email: myers@shgc.stanford.edu
          Primer A: ACAGGTGTGTTTTCATTTGC
          Primer B: GAGGAAAATGGTGCTTGA
          STS size: 150
          PCR Profile:
            Initial incubation: 94 degrees C for 90 seconds
            Denaturation: 94 degrees C for 15 seconds
            Annealing: 62 degrees C for 23 seconds
            Polymerization: 72 degrees C for 30 seconds
            PCR Cycles: 30
            Thermal Cycler: Perkin Elmer 9600
          Protocol:
            Template: 25 ng
            Primers: each 1 uM
            dNTPs: each 200 uM
            Taq Polymerase: 0.05 units/ul
            Total Vol: 10 ul
          Buffer:
            MgCl2: 2.5 mM
            KCl: 50 mM
            Tris-HCl: 20 mM
            pH: 8.3
          Prepared with primer pairs derived from T16078--Merck/UniEST.
          Location/Qualifiers
        1..250
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
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/mmap="16"
primer_bind 10..159
primer_bind 10..30
primer_bind complement(140..159)
ORIGIN
Query Match 100.0%; Score 11; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
Db 31 CTTTGGCACTA 41

RESULT 47
LOCUS CQ675738/c 251 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 20664 from Patent WO02070737.
ACCESSION CQ675738
VERSION CQ675738.1 GI:42179569
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLES Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 20664 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source 1..251
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
Db 194 CTTTGGCACTA 184

RESULT 48
LOCUS BV084034 251 bp DNA linear STS 30-SEP-2003
DEFINITION sc1275_p3 NC350 Zea mays NC350 Zea mays STS genomic, sequence
tagged site.
ACCESSION BV084034
VERSION BV084034.1 GI:37055691
KEYWORDS STS.
SOURCE Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 251)
TITLES MPZ-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ATCTACCAATGCCCTCATATTT
Primer B: GTTGTAGCAGTACGCCAGTTCA
Protocol:

Primer B: GTTGTAGCAGTACGCCAGTTCA
Protocol:
PCR amplification of genomic DNA
Template: 50 ng each 0.5 uM
Primer: each 200 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 62 69 56 49 49 49 50 50 55 60 52
49 57 34 34 35 44 44 44 51 56 56 56 51 74 70 71 71 69 71 71
72 73 71 71 73 73 71 73 88 90 85 74 69 75 58 57 57 62 58 54 59 63
61 55 55 66 55 55 60 54 54 55 55 55 71 72 78 60 61 57 55 55 55
60 60 66 74.

FEATURES
source 1..251
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="NC350"
/db_xref="taxon:4577"
/clone_lib="Zea mays NC350"
/dev_stage="seedling"
/notes="Organ: leaf; genomic DNA from inbred line"
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Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
Db 72 CTTTGGCACTA 82

RESULT 49
LOCUS BV084035 251 bp DNA linear STS 30-SEP-2003
DEFINITION sc1275_p3 Kull3 Zea mays Kull3 Zea mays STS genomic, sequence
tagged site.
ACCESSION BV084035
VERSION BV084035.1 GI:37055692
KEYWORDS STS.
SOURCE Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 251)
TITLES MPZ-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ATCTACCAATGCCCTCATATTT
Primer B: GTTGTAGCAGTACGCCAGTTCA
Protocol:

```

```

PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 55 59 54 49 49 53 53 50 50 55 59 54
54 39 39 25 25 25 51 51 56 71 71 77 73 72 67 70 66 66 71
71 71 71 71 73 81 73 76 66 66 66 66 60 60 60 66 60 66 70
69 71 64 64 59 67 66 54 54 55 55 55 66 66 70 60 64 58 55 55
55 55 55 61.

FEATURES
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Location/Qualifiers
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/cultivar="Kull3"
/db_xref="taxon:4577"
/clone_lib="Zea mays Kull3"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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STS
ORIGIN
Query Match 100.0%; Score 11; DB 11; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 72 CTTTGGCACTA 82

RESULT 50
BV084036
LOCUS
DEFINITION
sc1275_p3 Kull1 Zea mays Kull1 Zea mays STS genomic, sequence
tagged site.
ACCESSION
BV084036
VERSION
BV084036.1 GI:37055693
KEYWORDS
STS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 251)
AUTHORS
McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
TITLE
MPZ-UCI Joint SNP Discovery
JOURNAL
Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ATCCTACCAATGCCCTCATATTT
Primer B: GTTGTAGCAGTACAGCCAGTTCA
Protocol:
PCR amplification of genomic DNA
Template: 50 ng

```

```

Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 66 59 60 51 52 41 46 44 52 54 52 47
47 55 66 62 62 64 68 68 78 81 71 71 75 86 74 61 65 60 56 58 63
77 76 76 74 77 76 79 74 82 63 67 67 67 65 72 72 68 68 57 61 63
66 60 57 57 57 64 65 60 50 50 50 54 69 69 76 69 68 63 50 52 50
55 57 62 64.

FEATURES
source
Location/Qualifiers
1..251
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Kull1"
/db_xref="taxon:4577"
/clone_lib="Zea mays Kull1"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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STS
ORIGIN
Query Match 100.0%; Score 11; DB 11; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 72 CTTTGGCACTA 82

Search completed: March 12, 2005, 10:28:49
Job time : 1462 secs

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**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 07:00:47 ; Search time 235 Seconds  
(without alignments)  
277.094 Million cell updates/sec

Title: US-10-070-588A-112  
Perfect score: 11  
Sequence: 1 ctttggcacta 11

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	11	AAS02843	Aas02843 Human pre
C 2	11	100.0	11	AAS02842	Aas02842 Human pre
C 3	11	100.0	17	ACD64825	ACD64825 HCV minus
C 4	11	100.0	17	ACD57843	ACD57843 HCV DNaz
C 5	11	100.0	17	ACD57844	ACD57844 HCV DNaz
C 6	11	100.0	17	ACD64826	ACD64826 HCV minus
C 7	11	100.0	17	AD183295	AD183295 HCV DNaz
C 8	11	100.0	17	AD186768	AD186768 HCV DNaz
C 9	11	100.0	17	AD186767	AD186767 HCV DNaz
C 10	11	100.0	17	AD183296	AD183296 HCV DNaz
C 11	11	100.0	18	AH231171	AH231171 Nitric ox
C 12	11	100.0	22	AAH85553	AAH85553 PCR prime
C 13	11	100.0	23	AAH24199	AAH24199 PCR prime
C 14	11	100.0	33	AAH76792	AAH76792 Human bro
C 15	11	100.0	47	AAD38062	AAD38062 Maize pro
C 16	11	100.0	77	AA122229	AA122229 Probe #12
C 17	11	100.0	77	ABA67308	ABA67308 Human fo
C 18	11	100.0	77	AA147524	AA147524 Probe #16
C 19	11	100.0	77	ABA49398	ABA49398 Human bre
C 20	11	100.0	77	AAK41482	AAK41482 Human bon

21	11	100.0	77	4	AAK15744	Aak15744 Human bra
22	11	100.0	77	4	ABS41072	Abs41072 Human liv
23	11	100.0	77	5	AAI07928	Aai07928 Probe #79
24	11	100.0	77	6	ABS15487	Abs15487 Human gen
25	11	100.0	100	3	AAK22084	Aak22084 Human sec
26	11	100.0	121	6	ABK26046	Abk26046 Amino aci
27	11	100.0	121	6	ABK26045	Abk26045 Amino aci
28	11	100.0	121	12	ADN44736	Adn44736 Mutant ce
29	11	100.0	121	12	ADN44737	Adn44737 Mutant ce
30	11	100.0	153	4	AAI23415	Aai23415 Probe #13
31	11	100.0	153	4	ABA68523	Abag68523 Human foe
32	11	100.0	153	4	AAI48735	Aai48735 Probe #17
33	11	100.0	153	4	ABA50565	Abas50565 Human bre
34	11	100.0	153	4	ABA35504	Aba35504 Probe #13
35	11	100.0	153	4	AAK42661	Aak42661 Human bon
36	11	100.0	153	4	AAK16890	Aak16890 Human bra
37	11	100.0	153	4	ABS42283	Abs42283 Human liv
38	11	100.0	153	5	AAI09041	Aai09041 Probe #90
39	11	100.0	153	6	ABS16713	Abs16713 Human gen
40	11	100.0	204	8	ACF72987	Acf72987 Staphyloc
41	11	100.0	213	6	ABS68966	Abs68966 Novel mur
42	11	100.0	240	6	ABL71901	Ab171901 Corn tass
43	11	100.0	245	5	ABA11368	Abal11368 Human nar
44	11	100.0	246	6	ABN24053	Abn24053 Human ORF
45	11	100.0	255	5	AAH81973	Aah81973 Rat diffe
46	11	100.0	256	7	ADS68954	Ads68954 Corn seed
47	11	100.0	273	6	ABQ67322	Abq67322 Listeria
48	11	100.0	276	3	AAK23036	Aak23036 Human sec
49	11	100.0	284	4	AAI23068	Aai23068 Human bre
50	11	100.0	286	4	AAK506829	Aak506829 Human can
51	11	100.0	290	4	AAK58491	Aak58491 Human imm
52	11	100.0	293	4	AAK60256	Aak60256 Human can
53	11	100.0	294	8	ACA37530	ACA37530 Prokaryot
54	11	100.0	297	6	ABL85556	Ab185556 Human ova
55	11	100.0	301	2	AAQ27769	Aaq27769 Heat-resi
56	11	100.0	303	4	AAH24197	Aah24197 Mouse age
57	11	100.0	308	6	ABQ56040	Abq56040 Human ova
58	11	100.0	309	4	AAI23110	Aai23110 Probe #13
59	11	100.0	309	4	ABA68199	Aba68199 Human foe
60	11	100.0	309	4	AAI48413	Aai48413 Probe #17
61	11	100.0	309	4	ABA50256	Abas50256 Human bre
62	11	100.0	309	4	ABA35210	Aba35210 Probe #13
63	11	100.0	309	4	AAK42333	Aak42333 Human bon
64	11	100.0	309	4	AAK16579	Aak16579 Human bra
65	11	100.0	309	4	ABS41948	Abs41948 Human liv
66	11	100.0	309	5	AAI08760	Aai08760 Probe #87
67	11	100.0	309	6	ABS16392	Abs16392 Human gen
68	11	100.0	314	4	AAK60943	Aak60943 Human can
69	11	100.0	321	10	ADF00678	Adf00678 Bacterial
70	11	100.0	325	12	ACH90211	Ach90211 Human gen
71	11	100.0	329	4	AAH50678	Aah50678 Human tum
72	11	100.0	332	4	AAK24505	Aak24505 Human ova
73	11	100.0	333	6	ABN25437	Abn25437 Human ORP
74	11	100.0	341	3	AAK03627	Aak03627 Human sec
75	11	100.0	342	5	AAH83113	Aah83113 Human ova
76	11	100.0	353	3	ADF56998	Adf56998 Urogenita
77	11	100.0	355	5	ABV17449	Abv17449 Human pro
78	11	100.0	357	10	ABZ40917	Abz40917 N. gonorr
79	11	100.0	359	4	AAI14206	Aai14206 Human bre
80	11	100.0	360	6	ABN77089	Abn77089 Human ORF
81	11	100.0	365	4	AAI14209	Aai14209 Probe #41
82	11	100.0	365	4	ABA55935	Abas55935 Human foe
83	11	100.0	365	4	AAI35590	Aai35590 Probe #42
84	11	100.0	365	4	ABA45437	Abas45437 Human bre
85	11	100.0	365	4	AAK25602	Aak25602 Probe #40
86	11	100.0	365	4	AAK29630	Aak29630 Human bon
87	11	100.0	365	4	AAK04148	Aak04148 Human bra
88	11	100.0	365	4	ABS29267	Abs29267 Human liv
89	11	100.0	365	5	AAI04045	Aai04045 Probe #40
90	11	100.0	365	6	ABS04186	Abas04186 Human gen
91	11	100.0	366	10	ABZ40921	Abz40921 N. gonorr
92	11	100.0	372	10	ACF70960	Acf70960 Photorhab
93	11	100.0	376	3	ADF57075	Adf57075 Urogenita

94	11	100.0	378	9	ADB09445	Adb09445 Alloiococ	C 167	11	100.0	478	4	AAI19424	Aai19424 Probe #93
95	11	100.0	378	9	ADB09447	Adb09447 Alloiococ	C 168	11	100.0	478	4	ABA64437	AbA64437 Human foe
96	11	100.0	382	4	AAH35668	Aah35668 Human col	C 169	11	100.0	478	4	AAI44612	Aai44612 Probe #13
97	11	100.0	393	6	ABL87541	AbL87541 Human ova	C 170	11	100.0	478	4	ABA46574	AbA46574 Human bre
98	11	100.0	396	4	AAF94839	Aaf94839 Human ova	C 171	11	100.0	478	4	ABA31573	AbA31573 Probe #10
99	11	100.0	396	6	ABL48789	AbL48789 Ovarian c	C 172	11	100.0	478	4	AAK38623	Aak38623 Human bon
100	11	100.0	396	6	ABT03106	Abt03106 Human ova	C 173	11	100.0	478	4	AAK12894	Aak12894 Human bra
101	11	100.0	396	11	ADM10699	Adm10699 Human ova	C 174	11	100.0	478	4	ABs38188	AbS38188 Human liv
102	11	100.0	396	12	ADJ11029	Adj11029 Represent	C 175	11	100.0	478	5	AAI05149	Aai05149 Probe #51
103	11	100.0	396	12	ADM43290	Adm43290 Human ova	C 176	11	100.0	478	6	ABs12690	AbS12690 Human gen
104	11	100.0	404	4	AAK61967	Aak61967 Human imm	C 177	11	100.0	478	9	ACH47793	Ach47793 Human inf
105	11	100.0	412	8	ACH30318	Ach30318 Human tes	C 178	11	100.0	478	10	ADeB2223	ADeB2223 Arabidops
106	11	100.0	422	8	ABX53229	Abx53229 Bovine ES	C 179	11	100.0	479	9	ACH35102	Ach35102 Human end
107	11	100.0	423	4	AAI13892	Aai13892 Probe #38	C 180	11	100.0	479	10	ACD93599	ACd93599 Human col
108	11	100.0	423	4	ABs55600	AbS55600 Human foe	C 181	11	100.0	481	4	AAI13802	Aai13802 Probe #37
109	11	100.0	423	4	AAI35254	Aai35254 Probe #39	C 182	11	100.0	481	4	AAI35162	Aai35162 Probe #38
110	11	100.0	423	4	ABA45119	AbA45119 Human bre	C 183	11	100.0	481	4	ABs28826	AbS28826 Human liv
111	11	100.0	423	4	ABs25297	AbS25297 Probe #37	C 184	11	100.0	481	5	AAI03676	Aai03676 Probe #36
112	11	100.0	423	4	AAK29293	Aak29293 Human bon	C 185	11	100.0	484	9	ACH35805	Ach35805 Human end
113	11	100.0	423	4	AAK03827	Aak03827 Human bra	C 186	11	100.0	486	5	ABV11494	ABv11494 Human pro
114	11	100.0	423	4	ABs28919	AbS28919 Human liv	C 187	11	100.0	487	4	AAI01690	Aai01690 Human rep
115	11	100.0	423	5	AAI03756	Aai03756 Probe #37	C 188	11	100.0	489	5	ABV60003	ABv60003 Human pro
116	11	100.0	423	5	AAO2900	AAo2900 DNA encod	C 189	11	100.0	493	12	ADOS5078	ADoS5078 Gene #175
117	11	100.0	423	6	ABs03855	AbS03855 Human gen	C 190	11	100.0	495	4	AA553839	AA553839 Helicobac
118	11	100.0	425	12	ADP95751	ADp95751 Cotton ex	C 191	11	100.0	495	5	ABV56227	ABv56227 Human pro
119	11	100.0	434	8	ABx53729	ABx53729 Bovine BS	C 192	11	100.0	495	12	ADQ34558	ADQ34558 Human SLI
120	11	100.0	438	9	ACI21273	ACi21273 DNA clone	C 193	11	100.0	497	8	ABZ52714	ABZ52714 Aspergill
121	11	100.0	443	3	ADF57455	ADf57455 Urogenita	C 194	11	100.0	499	8	ABZ52947	ABZ52947 Aspergill
122	11	100.0	444	6	AAO38058	AAo38058 Maize rib	C 195	11	100.0	502	4	AAI34729	Aai34729 Human mus
123	11	100.0	444	12	ADQ63122	ADQ63122 Transcrip	C 196	11	100.0	502	8	ABX57717	ABx57717 cDNA enco
124	11	100.0	445	5	ABV37976	ABv37976 Human pro	C 197	11	100.0	502	12	ADJ27444	ADj27444 Human mus
125	11	100.0	446	5	ABV32639	ABv32639 Human pro	C 198	11	100.0	506	9	ACL21285	ACL21285 DNA clone
126	11	100.0	448	6	ABL80271	ABl80271 Human ova	C 199	11	100.0	511	3	AC98705	ACe98705 Human col
127	11	100.0	451	13	ADR26621	ADr26621 Breast ca	C 200	11	100.0	511	12	ACH67989	ACH67989 Arabidops
128	11	100.0	455	6	ABL63578	ABl63578 Breast ca	C 201	11	100.0	518	10	ADe81299	ADe81299 Arabidops
129	11	100.0	456	4	AAI12991	Aai12991 Probe #29	C 202	11	100.0	519	6	ABV98170	ABv98170 Human pro
130	11	100.0	456	4	ABs45492	AbS45492 Human foe	C 203	11	100.0	525	5	ABV51300	ABv51300 Human pan
131	11	100.0	456	4	AAI34348	Aai34348 Probe #30	C 204	11	100.0	525	10	ADD49609	ADd49609 Human lun
132	11	100.0	456	4	ABs44244	AbS44244 Human bre	C 205	11	100.0	530	11	ADT97846	ADt97846 Colton can
133	11	100.0	456	4	AAK28424	Aak28424 Human bon	C 206	11	100.0	531	4	AAK71000	Aak71000 Human imm
134	11	100.0	456	4	AAK02978	AAk02978 Human bra	C 207	11	100.0	531	6	ABL55589	ABl55589 HCV bait
135	11	100.0	456	4	ABs28020	AbS28020 Human liv	C 208	11	100.0	532	13	ACN61789	ACn61789 Cotton gy
136	11	100.0	456	5	AAI02909	Aai02909 Probe #29	C 209	11	100.0	550	11	ADT95733	ADt95733 Colton can
137	11	100.0	456	5	ABV47243	ABv47243 Human pro	C 210	11	100.0	551	2	Az222865	Az222865 Rice phos
138	11	100.0	456	6	ABs02932	AbS02932 Human gen	C 211	11	100.0	551	12	ACH76511	ACH76511 Human gen
139	11	100.0	457	4	AAI02856	Aai02856 Human rep	C 212	11	100.0	552	10	ADH83244	ADh83244 Enterococ
140	11	100.0	459	10	ACF71181	ACf71181 Photorthab	C 213	11	100.0	554	4	AAH31949	Aah31949 Human oli
141	11	100.0	460	8	ABx45697	ABx45697 Bovine ES	C 214	11	100.0	556	6	ABT10525	ABt10525 Human bre
142	11	100.0	460	11	ACN90123	ACn90123 Breast ca	C 215	11	100.0	560	13	ADQ58471	ADq58471 Novel can
143	11	100.0	462	4	AAI12348	Aai12348 Probe #22	C 216	11	100.0	561	5	ABV60313	ABv60313 Human pro
144	11	100.0	462	4	ABs45049	AbS45049 Human foe	C 217	11	100.0	561	6	ABQ57829	ABq57829 Human col
145	11	100.0	462	4	AAI33703	Aai33703 Probe #23	C 218	11	100.0	564	4	AAI05701	Aai05701 Human rep
146	11	100.0	462	4	ABs43598	AbS43598 Human bre	C 219	11	100.0	564	13	ACN60377	ACn60377 Cotton gy
147	11	100.0	462	4	ABA23801	ABa23801 Probe #22	C 220	11	100.0	565	6	ABK62144	ABk62144 Rat seque
148	11	100.0	462	4	AAK27766	Aak27766 Human bon	C 221	11	100.0	565	10	ADBS5123	ADbS5123 Toxicity-
149	11	100.0	462	4	AAK02322	AAk02322 Human bra	C 222	11	100.0	565	10	ADb49652	ADb49652 Primary r
150	11	100.0	462	4	ABs27346	AbS27346 Human liv	C 223	11	100.0	565	10	ADb49652	ADb49652 Primary r
151	11	100.0	462	5	AAI02260	Aai02260 Probe #22	C 224	11	100.0	566	2	AAI19858	Aai19858 Human gen
152	11	100.0	462	6	ABs02218	AbS02218 Human gen	C 225	11	100.0	569	9	ACL21280	ACL21280 DNA clone
153	11	100.0	467	6	ABL79801	ABl79801 Human ova	C 226	11	100.0	570	9	ACA62943	ACA62943 A. quisequ
154	11	100.0	468	4	AAI10128	Aai10128 Probe #61	C 227	11	100.0	571	9	ACL21295	ACL21295 DNA clone
155	11	100.0	468	4	ABs1758	ABs1758 Human foe	C 228	11	100.0	573	3	RAF09475	RAF09475 Fusarium
156	11	100.0	468	4	AAI13174	Aai13174 Probe #60	C 229	11	100.0	573	12	ADM32020	ADM32020 Vaccinia
157	11	100.0	468	4	ABs21586	AbS21586 Probe #52	C 230	11	100.0	573	12	ADM32021	ADM32021 Vaccinia
158	11	100.0	468	4	AAK25504	Aak25504 Human bon	C 231	11	100.0	573	12	ADM32022	ADM32022 Vaccinia
159	11	100.0	468	4	AAK00065	Aak00065 Human bon	C 232	11	100.0	573	12	ADM32019	ADM32019 Vaccinia
160	11	100.0	468	4	ABs25072	ABs25072 Human liv	C 233	11	100.0	574	13	ACN60436	ACn60436 Cotton gy
161	11	100.0	468	5	AAI00069	Aai00069 Probe #60	C 234	11	100.0	574	12	ADM32028	ADM32028 Vaccinia
162	11	100.0	468	6	ABs00070	ABs00070 Human gen	C 235	11	100.0	575	12	ADJ74919	ADj74919 Marker ge
163	11	100.0	471	6	ABT10410	ABt10410 Human bre	C 236	11	100.0	575	12	ADM32031	ADM32031 Vaccinia
164	11	100.0	472	4	AAI18795	Aai18795 Human bre	C 237	11	100.0	575	12	ADM32025	ADM32025 Vaccinia
165	11	100.0	472	4	AAI1031	AAi1031 Human bre	C 238	11	100.0	575	12	ADM32026	ADM32026 Vaccinia
166	11	100.0	476	10	ADG37466	ADg37466 Aspergill	C 239	11	100.0	575	12	ADM32027	ADM32027 Vaccinia

c 240	11	100.0	575	12	ADM32033	Adm32033 Vaccinia	c 313	11	100.0	776	4	AAK62718	Aak62718 Human imm
c 241	11	100.0	575	12	ADM32034	Adm32034 Vaccinia	c 314	11	100.0	787	2	AAV74667	Aav74667 Staphyloc
c 242	11	100.0	575	12	ADM32032	Adm32032 Vaccinia	c 315	11	100.0	806	6	ABL92116	Abi92116 Human Tum
c 243	11	100.0	575	12	ADM32030	Adm32030 Vaccinia	c 316	11	100.0	806	10	ADE96293	Ade96293 Human uri
c 244	11	100.0	576	4	AAI18463	Aai18463 Probe #83	c 317	11	100.0	806	10	ABX72041	Abx72041 DNA encod
c 245	11	100.0	576	4	ABA63468	Abas63468 Human toe	c 318	11	100.0	812	2	AAV84439	Aav84439 Human sec
c 246	11	100.0	576	4	AAI43580	Aai43580 Probe #12	c 319	11	100.0	812	4	ABA83222	Abas83222 Human.sec
c 247	11	100.0	576	4	ABA30666	Abas30666 Probe #91	c 320	11	100.0	812	9	ACH04723	Ach04723 Novel Hum
c 248	11	100.0	576	4	AAK37706	Aak37706 Human bon	c 321	11	100.0	812	9	ACD44533	Acd44533 Human cDN
c 249	11	100.0	576	4	AAK12001	Aak12001 Human bra	c 322	11	100.0	813	4	AAH06511	Aah06511 Human cDN
c 250	11	100.0	576	4	ABS37356	Abs37356 Human liv	c 323	11	100.0	816	12	ADL02353	Adl02353 DNA encod
c 251	11	100.0	576	6	ABS11697	Abs11697 Human gen	c 324	11	100.0	824	6	ABN98948	Abn98948 Arabidops
c 252	11	100.0	577	9	ACL21287	ACL21287 DNA clone	c 325	11	100.0	847	2	AA77761	Aat77761 RIP fusio
c 253	11	100.0	579	3	AAAC56133	Aac56133 Eucalyptu	c 326	11	100.0	847	2	AA79869	Aat79869 Pro-ribo
c 254	11	100.0	579	12	ADM32024	Adm32024 Vaccinia	c 327	11	100.0	864	3	AAAC39809	Aac39809 Arabidops
c 255	11	100.0	580	6	ABN62287	Abn62287 Human can	c 328	11	100.0	866	2	AAAC39943	Aac39943 Gastric c
c 256	11	100.0	584	9	ACL21279	ACL21279 DNA clone	c 329	11	100.0	879	6	ABN66504	Abn66504 Streptoco
c 257	11	100.0	584	9	ACL21284	ACL21284 DNA clone	c 330	11	100.0	880	2	AAV88389	Aav88389 EST clone
c 258	11	100.0	585	11	ADT95500	Adt95500 Colon can	c 331	11	100.0	882	10	ADE96298	Ade96298 Human uri
c 259	11	100.0	585	12	ADM32023	Adm32023 Vaccinia	c 332	11	100.0	891	8	ACA33009	Aca33009 Prokaryot
c 260	11	100.0	588	3	AAAC32679	Aac32679 Arabidops	c 333	11	100.0	892	11	ACN84258	Acn84258 Breast ca
c 261	11	100.0	589	3	AAAC48522	Aac48522 Arabidops	c 334	11	100.0	894	4	AA553121	Aas553121 Enterococ
c 262	11	100.0	590	4	AAK11575	Aak11575 Human bra	c 335	11	100.0	909	6	AAAD38056	Aad38056 Maize pro
c 263	11	100.0	590	4	ABS37016	Abs37016 Human liv	c 336	11	100.0	910	2	AAQ58815	Aaq58815 NANBH vir
c 264	11	100.0	594	12	ADM32029	Adm32029 Vaccinia	c 337	11	100.0	910	12	ADJ81661	Adj81661 Non-A-non
c 265	11	100.0	595	9	ACL21278	ACL21278 DNA clone	c 338	11	100.0	920	4	AAAS32972	Aas32972 DNA encod
c 266	11	100.0	597	6	ABQ58934	Abq58934 Human col	c 339	11	100.0	937	2	AAAT13899	Aat13899 HCV E2 an
c 267	11	100.0	598	9	ACL21297	ACL21297 DNA clone	c 340	11	100.0	944	2	AAAT78475	Aat78475 Maize RIP
c 268	11	100.0	600	12	ACH66952	Ach66952 Human gen	c 341	11	100.0	960	5	ADJ63592	Adj63592 Human ova
c 269	11	100.0	605	10	ADC58601	Adc58601 Mouse cha	c 342	11	100.0	966	4	AAH78733	Aah78733 Human HSK
c 270	11	100.0	608	9	ACL21303	ACL21303 DNA clone	c 343	11	100.0	966	4	AAAL35410	Aal35410 Human mus
c 271	11	100.0	611	6	ABQ57631	Abq57631 Human col	c 344	11	100.0	966	8	ABX58398	Abx58398 cDNA enco
c 272	11	100.0	616	10	ADB57338	Adb57338 Toxicity-	c 345	11	100.0	966	12	ADJ28125	Adj28125 Human mus
c 273	11	100.0	621	11	ADT95306	Adt95306 Colon can	c 346	11	100.0	969	8	ACA29512	Aca29512 Prokaryot
c 274	11	100.0	623	2	AAAL3322	Aal3322 Enterococ	c 347	11	100.0	978	2	AAQ20478	Aaq20478 Maize RIP
c 275	11	100.0	623	6	ABQ599317	Abq599317 Enterococ	c 348	11	100.0	978	2	AAAT77756	Aat77756 RIP fusio
c 276	11	100.0	623	8	ACA28837	Aca28837 Prokaryot	c 349	11	100.0	978	2	AAAT79864	Aat79864 Truncated
c 277	11	100.0	625	9	ACL21293	ACL21293 DNA clone	c 350	11	100.0	984	2	AAAT79863	Aat79863 Single ch
c 278	11	100.0	625	9	ACL21286	ACL21286 DNA clone	c 351	11	100.0	985	2	AAAT77755	Aat77755 RIP fusio
c 279	11	100.0	627	6	ABN62314	Abn62314 Human can	c 352	11	100.0	986	2	AAAT77757	Aat77757 RIP fusio
c 280	11	100.0	629	13	ACN45781	Acn45781 Cotton pr	c 353	11	100.0	986	2	AAAT79865	Aat79865 Truncated
c 281	11	100.0	634	6	ABN62315	Abn62315 Human can	c 354	11	100.0	987	2	AAQ20479	Aaq20479 Maize RIP
c 282	11	100.0	635	5	ABV55241	Abv55241 Human pro	c 355	11	100.0	987	2	AAAT78467	Aat78467 Maize KRI
c 283	11	100.0	636	5	AA567558	Aas67558 DNA encod	c 356	11	100.0	993	8	ACA52689	Aca52689 Prokaryot
c 284	11	100.0	636	6	ABK62315	Abk62315 Rat sequ	c 357	11	100.0	1001	4	AAAF91445	Aaf91445 Haemophil
c 285	11	100.0	636	12	ADP71597	Adp71597 Renal tox	c 358	11	100.0	1001	6	ABK37825	Abk37825 DNA sequ
c 286	11	100.0	641	9	ACL21294	ACL21294 DNA clone	c 359	11	100.0	1002	2	AAAX85552	Aax85552 Probe der
c 287	11	100.0	643	13	ACN46467	Acn46467 Cotton pr	c 360	11	100.0	1002	2	AAAX85551	Aax85551 cDNA of a
c 288	11	100.0	648	12	ACH91604	Ach91604 Human gen	c 361	11	100.0	1029	2	AAAT77754	Aat77754 RIP fusio
c 289	11	100.0	652	3	AAF15615	Aaf15615 Human pro	c 362	11	100.0	1032	12	ADL81763	Adl81763 P. aerugi
c 290	11	100.0	652	4	AAF72780	Aaf72780 Human pro	c 363	11	100.0	1029	2	AAAT79862	Aat79862 Maize gin
c 291	11	100.0	654	2	AAH87388	Aah87388 Human sin	c 364	11	100.0	1049	12	ADI34872	Adi34872 Human RAB
c 292	11	100.0	668	4	AA556408	Aas56408 Human cDN	c 365	11	100.0	1050	5	AAAS91757	Aas91757 DNA encod
c 293	11	100.0	669	11	ACN81228	Acn81228 Breast ca	c 366	11	100.0	1053	2	AAAT78473	Aat78473 Maize RIP
c 294	11	100.0	677	3	AAA63869	Aaa63869 cDNA sequ	c 367	11	100.0	1053	6	ABZ32465	Abz32465 Candida a
c 295	11	100.0	678	9	ACL21282	ACL21282 DNA clone	c 368	11	100.0	1059	2	AAAT78470	Aat78470 Maize RIP
c 296	11	100.0	678	10	ADH83245	Adh83245 Enterococ	c 369	11	100.0	1065	12	ADN72332	Adn72332 Thale cre
c 297	11	100.0	697	9	ACL21288	ACL21288 DNA clone	c 370	11	100.0	1071	10	ABX07389	Abx07389 S. pneumo
c 298	11	100.0	722	6	ABT09231	Abt09231 Phase-1 R	c 371	11	100.0	1074	2	AAAT79873	Aat79873 Maize rib
c 299	11	100.0	722	12	ADH22909	Adh22909 Partial D	c 372	11	100.0	1076	2	AAQ20476	Aaq20476 Maize pro
c 300	11	100.0	741	4	AAAS31370	Aas31370 Human cDN	c 373	11	100.0	1076	2	AAAT77753	Aat77753 proRIP co
c 301	11	100.0	741	5	ABA13461	Abas13461 Human ner	c 374	11	100.0	1076	2	AAAT79861	Aat79861 Maize pro
c 302	11	100.0	741	6	ABQ66694	Abq66694 Human pol	c 375	11	100.0	1083	10	ADH83222	Adh83222 Enterococ
c 303	11	100.0	741	10	ADC10716	Adc10716 Human cDN	c 376	11	100.0	1083	10	ACF67543	Acf67543 Photorhab
c 304	11	100.0	750	6	ABK49386	Abk49386 Hepatitis	c 377	11	100.0	1083	13	ADT43657	Adt43657 Bacterial
c 305	11	100.0	750	6	ADJ38057	Adj38057 Maize pro	c 378	11	100.0	1099	3	AAA96894	Aaa96894 Nucleotid
c 306	11	100.0	756	10	ACF67928	Acf67928 Photorhab	c 379	11	100.0	1102	2	AAAX85550	Aax85550 cDNA of a
c 307	11	100.0	759	6	ABQ68270	Abq68270 Listeria	c 380	11	100.0	1105	2	AAQ20477	Aaq20477 Maize pro
c 308	11	100.0	760	3	ADD33618	Add33618 Mouse mit	c 381	11	100.0	1105	2	AAAT79872	Aat79872 Maize pro
c 309	11	100.0	760	3	AAAC36981	Aac36981 Arabidops	c 382	11	100.0	1111	4	AAAS27054	Aas27054 cDNA enco
c 310	11	100.0	766	13	ADR64606	Adr64606 Cotton cD	c 383	11	100.0	1111	10	ADB93232	Adb93232 Human cDN
c 311	11	100.0	771	4	AAH07272	Aah07272 Human cDN	c 384	11	100.0	1113	3	ADR91780	Adr91780 Novel S.
c 312	11	100.0	775	10	ADD33621	Add33621 Mouse mit	c 385	11	100.0	1114	4	AAAS27473	Aas27473 cDNA enco

C 386	11	100.0	1114	10	ADB93651	Human CDN	Adb93651	459	11	100.0	1510	6	AA517397	AA517397	CDNA enco
C 387	11	100.0	1125	10	ADH83528	Enterococ	Adh83528	460	11	100.0	1515	8	ACA38885	ACA38885	Prokaryot
C 388	11	100.0	1132	13	AQ087663	Human tum	Aq087663	c 461	11	100.0	1537	3	AA36394	AA36394	Arabidops
C 389	11	100.0	1132	13	ACN39543	Tumour-as	Acn39543	462	11	100.0	1569	13	ADQ94299	ADQ94299	Arabidops
C 390	11	100.0	1161	2	AAQ20480	Maize RIP	Aaq20480	463	11	100.0	1575	3	AA335960	AA335960	Arabidops
C 391	11	100.0	1161	2	AAT77758	RIP fusio	Aat77758	464	11	100.0	1587	12	ADL03010	ADL03010	DNA enco
C 392	11	100.0	1161	2	AAT79866	Pro-ribo	Aat79866	465	11	100.0	1596	8	ACA33158	ACA33158	Prokaryot
C 393	11	100.0	1164	12	ADN74256	Thale cre	Adn74256	466	11	100.0	1611	12	ADL04211	ADL04211	DNA enco
C 394	11	100.0	1167	12	ADN04795	Antipsori	Adn04795	c 467	11	100.0	1656	13	ACN38176	ACN38176	Tumour-as
C 395	11	100.0	1167	13	ADP55197	Human PRO	Adp55197	c 468	11	100.0	1663	3	AAQ78055	AAQ78055	Human can
C 396	11	100.0	1167	13	ADR66261	Human pro	Adr66261	c 469	11	100.0	1683	2	AAQ20482	AAQ20482	Maize RIP
C 397	11	100.0	1167	13	ADR66603	Human pro	Adr66603	c 470	11	100.0	1683	2	AAT77760	AAT77760	RIP fusio
C 398	11	100.0	1167	13	ADR66186	Human pro	Adr66186	c 471	11	100.0	1683	2	AAT79868	AAT79868	Pro-ribo
C 399	11	100.0	1174	4	AAK74229	Human imm	Aak74229	c 472	11	100.0	1690	13	ADR26149	ADR26149	Breast ca
C 400	11	100.0	1174	4	AAK66156	Human imm	Aak66156	c 473	11	100.0	1695	2	AAT77762	AAT77762	RIP fusio
C 401	11	100.0	1174	4	AAK66159	Human imm	Aak66159	c 474	11	100.0	1695	2	AAT79870	AAT79870	Pro-ribo
C 402	11	100.0	1174	4	AAK74228	Human imm	Aak74228	c 475	11	100.0	1696	5	ADM19525	ADM19525	Novel hum
C 403	11	100.0	1174	4	AAK74227	Human imm	Aak74227	c 476	11	100.0	1698	11	ADM03470	ADM03470	Human CDN
C 404	11	100.0	1174	4	AAK66155	Human imm	Aak66155	477	11	100.0	1706	2	AAQ28232	AAQ28232	DNA enco
C 405	11	100.0	1174	5	ABA18478	Human ner	Abal8478	478	11	100.0	1713	4	AAK90386	AAK90386	Human dig
C 406	11	100.0	1174	5	ABA18480	Human ner	Abal8480	479	11	100.0	1713	4	AAK90385	AAK90385	Human dig
C 407	11	100.0	1174	5	ABA18479	Human ner	Abal8479	480	11	100.0	1713	5	AAAS39943	AAAS39943	Genomic s
C 408	11	100.0	1204	10	ADE96294	Human uri	Ade96294	481	11	100.0	1713	5	AAAS39940	AAAS39940	Genomic s
C 409	11	100.0	1207	2	AAQ40332	Sequence	Aaq40332	482	11	100.0	1713	6	ABK12470	ABK12470	Sperm rec
C 410	11	100.0	1207	2	AAQ40331	Sequence	Aaq40331	483	11	100.0	1713	9	ADB32900	ADB32900	Human nov
C 411	11	100.0	1216	5	AAH76788	Human bro	Aah76788	484	11	100.0	1713	9	ADB32903	ADB32903	Human nov
C 412	11	100.0	1219	2	AAV53637	Contig 26	Aav53637	485	11	100.0	1721	11	ADM03308	ADM03308	Human CDN
C 413	11	100.0	1219	2	AAV53352	DNA enco	Aav53352	c 486	11	100.0	1722	2	AAT77763	AAT77763	RIP fusio
C 414	11	100.0	1219	2	AAQ00904	Human des	Aax00904	c 487	11	100.0	1722	2	AAT79871	AAT79871	Pro-ribo
C 415	11	100.0	1219	2	AAV82636	Contig 26	Aav82636	c 488	11	100.0	1740	12	ADOS5217	ADOS5217	Human bla
C 416	11	100.0	1219	3	AAA14588	Nucleotid	Aaa14588	c 489	11	100.0	1748	2	AAK08944	AAK08944	Fragment
C 417	11	100.0	1219	3	AAA09447	Human con	Aaa09447	c 490	11	100.0	1752	6	ABZ13769	ABZ13769	Arabidops
C 418	11	100.0	1219	3	AAK49933	Human del	Aak49933	c 491	11	100.0	1752	6	ABA90328	ABA90328	Human poi
C 419	11	100.0	1219	6	ABS76707	Human del	Abs76707	c 492	11	100.0	1752	8	ACF72988	ACF72988	Staphyloc
C 420	11	100.0	1219	6	ABS71820	Human des	Abs71820	c 493	11	100.0	1752	13	ACN37607	ACN37607	Tumour-as
C 421	11	100.0	1226	3	AAAC55011	Arabidops	Aac55011	c 494	11	100.0	1766	10	ADG32798	ADG32798	Human DNA
C 422	11	100.0	1227	3	AAAC32944	Arabidops	Aac32944	c 495	11	100.0	1766	12	ADP03057	ADP03057	Human hou
C 423	11	100.0	1233	6	ABN98266	Arabidops	Abn98266	c 496	11	100.0	1766	13	ADQ84544	ADQ84544	Human tum
C 424	11	100.0	1244	2	AAK78479	Maize RIP	Aak78479	c 497	11	100.0	1766	13	ACN39866	ACN39866	Tumour-as
C 425	11	100.0	1245	2	AAQ97306	Pancrati	Aaq97306	c 498	11	100.0	1766	13	ADS88555	ADS88555	Human hou
C 426	11	100.0	1245	2	AAV40687	Human pan	Aav40687	c 499	11	100.0	1775	13	ADS47680	ADS47680	Bacterial
C 427	11	100.0	1262	12	ADQ23233	Human sof	Adq23233	c 500	11	100.0	1775	13	ADS47681	ADS47681	Bacterial
C 428	11	100.0	1263	10	ADF03464	Bacterial	Adf03464	c 501	11	100.0	1787	8	ACC62281	ACC62281	Human NOV
C 429	11	100.0	1266	12	ADJ10451	DNA of th	Adj10451	c 502	11	100.0	1791	3	AAK76102	AAK76102	Human ORF
C 430	11	100.0	1275	8	ADA70826	Rice gene	Ada70826	503	11	100.0	1791	6	ABK73785	ABK73785	Bacillus
C 431	11	100.0	1290	3	AAK48859	Arabidops	Aak48859	504	11	100.0	1799	3	AAQ97798	AAQ97798	Clone pre
C 432	11	100.0	1293	10	ACF68660	Photornab	Acf68660	505	11	100.0	1808	3	AAQ50417	AAQ50417	Arabidops
C 433	11	100.0	1296	2	AAK85549	CDNA of a	Aak85549	c 506	11	100.0	1810	12	ADQ64635	ADQ64635	Novel hum
C 434	11	100.0	1296	4	ABL11827	Drosophil	Abi11827	c 507	11	100.0	1811	3	AAAC34909	AAAC34909	Arabidops
C 435	11	100.0	1296	9	ADB07547	Alloiooc	Adb07547	c 508	11	100.0	1819	12	ADL83303	ADL83303	Human PRO
C 436	11	100.0	1299	8	ACA379022	Prokaryot	Ac379022	c 509	11	100.0	1825	4	ABL23579	ABL23579	Drosophil
C 437	11	100.0	1320	8	ACA28053	Prokaryot	Ac28053	c 510	11	100.0	1826	2	AAK08945	AAK08945	Fragment
C 438	11	100.0	1337	3	AAK48518	Arabidops	Aak48518	c 511	11	100.0	1826	10	ADB75369	ADB75369	Prostate
C 439	11	100.0	1355	3	AAK298183	Human sig	Aak298183	c 512	11	100.0	1826	10	ADB31337	ADB31337	Bicalutam
C 440	11	100.0	1357	5	ABV30252	Human pro	Abv30252	c 513	11	100.0	1826	13	ADN25537	ADN25537	Breast ca
C 441	11	100.0	1365	10	ACF04840	Wheat hom	Acf04840	c 514	11	100.0	1826	13	ACN41058	ACN41058	Tumour-as
C 442	11	100.0	1375	13	ADR25080	Breast ca	Adr25080	c 515	11	100.0	1826	13	ADP23323	ADP23323	PRO polyp
C 443	11	100.0	1389	12	ADL02819	DNA enco	Adl02819	c 516	11	100.0	1828	12	ADQ84185	ADQ84185	Human tum
C 444	11	100.0	1390	2	AAK85570	CDNA of a	Aak85570	c 517	11	100.0	1832	4	AAF27705	AAF27705	Human tra
C 445	11	100.0	1392	8	ACA18507	Prokaryot	Ac18507	c 518	11	100.0	1833	5	ADM19262	ADM19262	Novel hum
C 446	11	100.0	1395	4	AAK52913	Enterococ	Aak52913	c 519	11	100.0	1845	12	ADJ10455	ADJ10455	DNA of th
C 447	11	100.0	1397	3	AAK41116	Arabidops	Aak41116	c 520	11	100.0	1850	10	ADL13026	ADL13026	A. goesyp
C 448	11	100.0	1398	2	AAV74973	Staphyloc	Aav74973	c 521	11	100.0	1851	4	ABL10591	ABL10591	Drosophil
C 449	11	100.0	1401	4	AAK51360	Enterococ	Aak51360	c 522	11	100.0	1862	4	AAF32779	AAF32779	Human sec
C 450	11	100.0	1422	2	AAQ20481	Maize RIP	Aaq20481	c 523	11	100.0	1866	5	AAK50309	AAK50309	DNA enco
C 451	11	100.0	1422	2	AAT77759	RIP fusio	Aat77759	c 524	11	100.0	1879	4	ABL21007	ABL21007	Drosophil
C 452	11	100.0	1422	2	AAK79867	Pro-ribo	Aak79867	c 525	11	100.0	1879	5	AAAD17209	AAAD17209	Drosophil
C 453	11	100.0	1431	9	ADA30537	DNA enco	Ada30537	c 526	11	100.0	1886	6	AAK51671	AAK51671	Signal pe
C 454	11	100.0	1434	8	ACA46117	Prokaryot	Ac46117	c 527	11	100.0	1902	4	AAF86368	AAF86368	Murine Mi
C 455	11	100.0	1443	6	ABZ78274	A. niger	Abz78274	528	11	100.0	1922	10	ADC51631	ADC51631	Babesia g
C 456	11	100.0	1443	6	ABZ78237	A. niger	Abz78237	c 529	11	100.0	1926	4	AAF72755	AAF72755	Human pro
C 457	11	100.0	1443	6	ABA90327	Human pol	Ab90327	530	11	100.0	1926	10	ADF75254	ADF75254	Thale cre
C 458	11	100.0	1458	2	AAQ79936	Murine Ki	Aaq79936	c 531	11	100.0	1934	2	AAT42302	AAT42302	Maize rib



532	11	100.0	1937	12	ADQ97591	Adq97591 Mouse can	c 605	11	100.0	2396	10	ACF58208	Acf58208 B. antrac
533	11	100.0	1938	12	ADJ10453	Adj10453 DNA of th	c 606	11	100.0	2430	4	AAV26363	AAv26363 Moraxella
534	11	100.0	1943	5	ADL63188	Adl63188 Human ova	c 607	11	100.0	2455	2	ADJ40189	Adj40189 Plant cDN
535	11	100.0	1946	4	ABL03079	AbL03079 Drosophil	c 608	11	100.0	2463	12	ADJ40189	Adj40189 Plant cDN
536	11	100.0	1950	6	ABZ78217	Abz78217 A. niger	c 609	11	100.0	2470	10	ADF82213	Adf82213 Leukaemia
537	11	100.0	1951	2	AAQ94449	AAq94449 Bacterial	c 610	11	100.0	2483	10	ADC37612	Adc37612 Human nuc
538	11	100.0	1951	2	AAQ94507	AAq94507 Transferr	c 611	11	100.0	2491	6	ABQ60924	Abq60924 Human RNA
539	11	100.0	1951	2	AAZ89171	AAz89171 H. influe	c 612	11	100.0	2498	4	AAK82449	AAk82449 Human imm
540	11	100.0	1951	2	AAV21443	AAv21443 H. influe	c 613	11	100.0	2505	6	ABK89930	ABk89930 cDNA enco
541	11	100.0	1951	3	AAZ91005	AAz91005 H. influe	c 614	11	100.0	2507	4	ABL24860	ABl24860 Drosophil
542	11	100.0	1953	10	ADD46838	AdD46838 Rat gene	c 615	11	100.0	2517	12	ADJ10457	Adj10457 DNA of th
543	11	100.0	1953	10	ADE56291	AdE56291 Rat gene	c 616	11	100.0	2517	12	ADJ10457	Adj10457 DNA of th
544	11	100.0	1954	2	AAQ94450	AAq94450 Bacterial	c 617	11	100.0	2520	2	AAQ77884	AAq77884 Neural th
545	11	100.0	1954	5	AAZ89172	AAz89172 H. influe	c 618	11	100.0	2520	2	AAQ77884	AAq77884 Neural th
546	11	100.0	1955	2	AAZ89172	AAz89172 H. influe	c 619	11	100.0	2520	2	AAQ77884	AAq77884 Neural th
547	11	100.0	1955	2	AAZ89172	AAz89172 H. influe	c 620	11	100.0	2520	2	AAQ77884	AAq77884 Neural th
548	11	100.0	1955	2	AAZ89172	AAz89172 H. influe	c 621	11	100.0	2520	2	AAQ77884	AAq77884 Neural th
549	11	100.0	1955	3	AAZ91006	AAz91006 H. influe	c 622	11	100.0	2522	4	AAZ51266	AAz51266 Human RNA
550	11	100.0	1974	2	AAQ94448	AAq94448 Bacterial	c 623	11	100.0	2554	12	ADM18433	Adm18433 Human chr
551	11	100.0	1974	2	AAQ94506	AAq94506 Transferr	c 624	11	100.0	2562	3	AAA26725	AAA26725 Candida a
552	11	100.0	1974	2	AAZ89170	AAz89170 H. influe	c 625	11	100.0	2565	6	ABZ32307	ABz32307 Candida a
553	11	100.0	1974	2	AAZ89170	AAz89170 H. influe	c 626	11	100.0	2582	4	AAH18575	AAh18575 Human cDN
554	11	100.0	1974	3	AAZ91004	AAz91004 H. influe	c 627	11	100.0	2585	10	ADE96297	AdE96297 Human uri
555	11	100.0	1993	2	AAQ94447	AAq94447 Bacterial	c 628	11	100.0	2595	5	AAH12711	AAh12711 Rat bombe
556	11	100.0	1993	2	AAQ94447	AAq94447 Bacterial	c 629	11	100.0	2597	5	AAH12711	AAh12711 Rat bombe
557	11	100.0	1993	2	AAZ89169	AAz89169 H. influe	c 630	11	100.0	2598	10	ADC77668	AdC77668 Human 619
558	11	100.0	1993	2	AAZ89169	AAz89169 H. influe	c 631	11	100.0	2598	10	ADC77668	AdC77668 Human 619
559	11	100.0	1993	3	AAZ91003	AAz91003 H. influe	c 632	11	100.0	2620	6	ABQ99343	ABq99343 Human cod
560	11	100.0	2000	6	ABZ16599	ABz16599 Arabidops	c 633	11	100.0	2629	4	AAZ26026	AAz26026 Human cDN
561	11	100.0	2000	8	ADA73076	AdA73076 Rice gene	c 634	11	100.0	2629	8	ABX73367	ABx73367 Human nov
562	11	100.0	2000	8	ADA71457	AdA71457 Rice gene	c 635	11	100.0	2635	10	ACA56660	ACa56660 Human ser
563	11	100.0	2000	8	ADA71877	AdA71877 Rice gene	c 636	11	100.0	2635	12	ADI56456	Adi56456 Human pol
564	11	100.0	2000	8	ADA71877	AdA71877 Rice gene	c 637	11	100.0	2638	6	ABQ99586	ABq99586 Human cod
565	11	100.0	2000	8	ADA73137	AdA73137 Rice gene	c 638	11	100.0	2638	6	ABQ99586	ABq99586 Human cod
566	11	100.0	2000	12	ADJ41213	AdJ41213 Plant cDN	c 639	11	100.0	2642	10	ADG32924	ADg32924 Human DNA
567	11	100.0	2007	4	ABL07189	ABl07189 Drosophil	c 640	11	100.0	2664	9	ADA29066	ADa29066 DNA enco
568	11	100.0	2007	12	ADK16488	ADk16488 Nanoarcha	c 641	11	100.0	2700	12	ADP28448	ADp28448 Human sec
569	11	100.0	2055	13	ADP55653	ADp55653 Human PRO	c 642	11	100.0	2700	12	ADP28447	ADp28447 Human sec
570	11	100.0	2058	10	ADL62904	ADl62904 Human apo	c 643	11	100.0	2701	5	AAZ67720	AAz67720 DNA enco
571	11	100.0	2058	13	ADP24029	ADp24029 PRO poly	c 644	11	100.0	2713	4	AAK85252	AAk85252 Human imm
572	11	100.0	2070	12	ADL16362	ADl16362 PBPl16 ve	c 645	11	100.0	2722	3	AAZ59922	AAz59922 Human sec
573	11	100.0	2112	5	AAZ65041	AAz65041 DNA enco	c 646	11	100.0	2754	3	AAZ59922	AAz59922 Human sec
574	11	100.0	2120	2	AAQ51236	AAq51236 Plant NAD	c 647	11	100.0	2754	6	ABZ13981	ABz13981 Arabidops
575	11	100.0	2120	12	ADP04480	ADp04480 Sea squir	c 648	11	100.0	2754	8	ADA68022	ADa68022 Arabidops
576	11	100.0	2121	10	ADB62617	ADb62617 Human cDN	c 649	11	100.0	2754	12	ADN72372	ADn72372 Thale cre
577	11	100.0	2128	4	ABL24013	ABl24013 Drosophil	c 650	11	100.0	2773	6	ABZ51339	ABz51339 cDNA enco
578	11	100.0	2159	5	ABV24585	ABv24585 Human pro	c 651	11	100.0	2785	4	AAH14593	AAh14593 Human cDN
579	11	100.0	2163	4	ABR89338	ABr89338 Escherich	c 652	11	100.0	2790	10	ACF70024	ACf70024 Phototrab
580	11	100.0	2169	10	ADB63370	ADb63370 Human cDN	c 653	11	100.0	2803	12	ADI16283	Adi16283 Human nuc
581	11	100.0	2178	12	ADM29100	Adm29100 HCV and h	c 654	11	100.0	2828	11	ADM03100	Adm03100 Human cDN
582	11	100.0	2181	11	ADM03741	Adm03741 Human cDN	c 655	11	100.0	2830	4	AAH17837	AAh17837 Human cDN
583	11	100.0	2187	9	ACA64722	ACa64722 Staphyloc	c 656	11	100.0	2839	4	AAH16448	AAh16448 Human cDN
584	11	100.0	2187	9	ADA30229	ADa30229 DNA enco	c 657	11	100.0	2842	10	ADE96296	AdE96296 Human uri
585	11	100.0	2187	10	ADF43361	AdF43361 Staphyloc	c 658	11	100.0	2853	8	ACA23231	ACa23231 Prokaryot
586	11	100.0	2190	8	ACA46308	ACa46308 Prokaryot	c 659	11	100.0	2856	11	ABD11591	ABd11591 Pseudomon
587	11	100.0	2208	8	ACF72480	ACf72480 Staphyloc	c 660	11	100.0	2892	4	AAK85236	AAk85236 Human imm
588	11	100.0	2211	4	AAZ54911	AAz54911 Staphyloc	c 661	11	100.0	2892	4	AAK85235	AAk85235 Human imm
589	11	100.0	2274	11	ADM02241	Adm02241 Human cDN	c 662	11	100.0	2897	4	AAH14555	AAh14555 Human cDN
590	11	100.0	2287	11	ADI30779	Adi30779 Human cDN	c 663	11	100.0	2904	3	AAZ46114	AAz46114 Arabidops
591	11	100.0	2288	10	ADE96295	AdE96295 Human uri	c 664	11	100.0	2938	5	ADL45797	ADl45797 Human ova
592	11	100.0	2292	8	ABZ24969	ABz24969 Zinc fing	c 665	11	100.0	2943	2	AAV40704	AAv40704 Spo-rel c
593	11	100.0	2298	10	ADC90469	AdC90469 E. faeciu	c 666	11	100.0	2966	10	ADE58151	AdE58151 Rat gene
594	11	100.0	2307	12	ADQ64657	ADq64657 Novel hum	c 667	11	100.0	2966	10	ADE58151	AdE58151 Rat gene
595	11	100.0	2337	12	ADL16340	ADl16340 Bacillus	c 668	11	100.0	2976	6	ABN70173	ABn70173 Streptoco
596	11	100.0	2363	10	ADD46352	AdD46352 Human gen	c 669	11	100.0	2979	8	ACA50693	ACa50693 Prokaryot
597	11	100.0	2371	2	AAQ24477	AAq24477 Heat-resi	c 670	11	100.0	2979	12	ADJ40051	Adj40051 Plant cDN
598	11	100.0	2372	4	ABL21686	ABl21686 Drosophil	c 671	11	100.0	3027	4	AAZ31210	AAz31210 Human cDN
599	11	100.0	2379	8	ACA37067	ACa37067 Prokaryot	c 672	11	100.0	3027	6	ABQ66534	ABq66534 Human pol
600	11	100.0	2388	2	AAV84554	AAv84554 Human sec	c 673	11	100.0	3027	10	ADC10556	AdC10556 Human cDN
601	11	100.0	2388	4	ABR84337	ABr84337 Human sec	c 674	11	100.0	3035	4	AAH16041	AAh16041 Human cDN
602	11	100.0	2388	9	ACH04838	ACH04838 Novel hum	c 675	11	100.0	3035	10	ADB75284	ADb75284 Prostate
603	11	100.0	2388	9	ACD44648	ACd44648 Human cDN	c 676	11	100.0	3039	11	ACN43859	ACn43859 Human mRN
604	11	100.0	2393	13	ADS50918	ADs50918 Bacterial	c 677	11	100.0	3060	6	ABN59744	ABn59744 Novel hum

678	11	100.0	3070	4	ABL05830	Abi05830 Drosophil	c 751	11	100.0	4328	5	AAS42504	Aas42504 Human CDN
679	11	100.0	3078	8	ADD46798	Add46798 Human gen	c 752	11	100.0	4336	4	ABL11826	Abi11826 Drosophil
680	11	100.0	3088	10	ADS31020	Ads31020 Human gen	c 753	11	100.0	4423	10	AAL50321	Aal50321 Murine ig
c 681	11	100.0	3094	13	ADR08274	Adr08274 Full leng	c 754	11	100.0	4447	3	AAA90951	Aa90951 B. lactof
c 682	11	100.0	3106	4	AH72702	Aah72702 Human cer	c 755	11	100.0	4447	3	AAA90934	Aa90934 B. lactof
c 683	11	100.0	3106	5	ADL63236	Adl63236 Human ova	c 756	11	100.0	4447	6	ABL49734	Abi49734 Brevibact
c 684	11	100.0	3106	11	ACN91634	Acn91634 Breast ca	c 757	11	100.0	4447	6	ABL49733	Abi49733 Brevibact
c 685	11	100.0	3134	4	ABL09496	Abi09496 Drosophil	c 758	11	100.0	4447	6	ADL22583	Adl22583 B. lactof
c 686	11	100.0	3135	6	ABQ60937	Abq60937 RAB9-like	c 759	11	100.0	4447	6	ADL22582	Adl22582 B. lactof
c 687	11	100.0	3135	12	ADF43052	Adf43052 Human K10	c 760	11	100.0	4447	10	ADB66212	Adb66212 B. lactof
c 688	11	100.0	3151	4	AH41464	Aah1464 Human CDN	c 761	11	100.0	4450	8	ABT17806	Abt17806 Aspergill
c 689	11	100.0	3152	12	ADO35874	Ado35874 Novel mou	c 762	11	100.0	4505	8	ABT19620	Abt19620 Aspergill
c 690	11	100.0	3175	6	ABZ35351	Abz35351 Human gen	c 763	11	100.0	4531	5	ABV25119	Abv25119 Human pro
c 691	11	100.0	3287	2	AAK13297	Aax13297 Enterococ	c 764	11	100.0	4580	8	ABX71048	Abx71048 Novel hum
c 692	11	100.0	3287	6	ABE99092	Abse99092 Enterococ	c 765	11	100.0	4659	13	ADR07337	Adr07337 Full leng
c 693	11	100.0	3294	2	AAQ70179	Aaq70179 Sequence	c 766	11	100.0	4661	12	ADN05217	Adn05217 Antipsori
c 694	11	100.0	3355	12	ADG31195	Adg31195 Novel mou	c 767	11	100.0	4682	8	ABX71047	Abx71047 Novel hum
c 695	11	100.0	3398	5	AAS73705	Aas73705 DNA encod	c 768	11	100.0	4699	2	AAQ94442	Aaq94442 Bacterial
c 696	11	100.0	3460	2	AAV39131	Aav39131 Polypepti	c 769	11	100.0	4699	2	AAQ94442	Aaq94442 Bacterial
c 697	11	100.0	3460	4	AH233959	Aah233959 Human K10	c 770	11	100.0	4699	2	AAZ49500	Aaz49500 Transfer
c 698	11	100.0	3471	4	ABL22276	Abi22276 Drosophil	c 771	11	100.0	4699	2	AAZ89156	Aaz89156 H. influe
c 699	11	100.0	3495	4	AAS06755	Aas06755 Polynucle	c 772	11	100.0	4699	2	AAV21428	Aav21428 H. influe
c 700	11	100.0	3498	8	ACA44451	Aca44451 Prokaryot	c 773	11	100.0	4821	2	AAZ90998	Aaz90998 H. influe
c 701	11	100.0	3506	6	AAI64198	Aai64198 Rat CRF2a	c 774	11	100.0	4920	6	ABQ70975	Abq70975 Listeria
c 702	11	100.0	3506	12	ADQ62971	Adq62971 Novel hum	c 775	11	100.0	4924	10	ADC30190	Adc30190 Human nov
c 703	11	100.0	3522	10	ADF03508	Adf03508 Bacterial	c 776	11	100.0	5002	13	ADT05461	Adt05461 Haemophil
c 704	11	100.0	3540	13	ADR08224	Adr08224 Full leng	c 777	11	100.0	5009	2	AAQ94444	Aaq94444 Bacterial
c 705	11	100.0	3570	10	ADC35141	Adc35141 Human bre	c 778	11	100.0	5009	2	AAZ49502	Aaz49502 Transfer
c 706	11	100.0	3585	3	AAA35157	Aaa35157 Human ade	c 779	11	100.0	5009	2	AAZ89158	Aaz89158 H. influe
c 707	11	100.0	3585	3	AAF21279	Aaf21279 Human low	c 780	11	100.0	5009	2	AAV21430	Aav21430 H. influe
c 708	11	100.0	3585	6	ABA94920	Ab94920 Human ecN	c 781	11	100.0	5009	3	AAZ91000	Aaz91000 H. influe
c 709	11	100.0	3585	10	ABZ96973	Abz96973 Human nuc	c 782	11	100.0	5011	10	ADD31993	Add31993 Rat corti
c 710	11	100.0	3585	4	ABD20822	Abd20822 Human pul	c 783	11	100.0	5033	2	AAQ94443	Aaq94443 Bacterial
c 711	11	100.0	3586	11	ABZ23153	Abz23153 Nitric ox	c 784	11	100.0	5033	2	AAZ49501	Aaz49501 Transfer
c 712	11	100.0	3631	12	ADL72876	Adl72876 Anthrax v	c 785	11	100.0	5033	2	AAZ89157	Aaz89157 H. influe
c 713	11	100.0	3738	4	ABL01852	Abi01852 Drosophil	c 786	11	100.0	5033	2	AAV21429	Aav21429 H. influe
c 714	11	100.0	3748	12	ADQ22398	Adq22398 Human sof	c 787	11	100.0	5033	3	AAZ90999	Aaz90999 H. influe
c 715	11	100.0	3776	12	ADO36012	Ado36012 Novel mou	c 788	11	100.0	5070	4	ABL18819	Abi18819 Drosophil
c 716	11	100.0	3786	12	ADI34873	Adi34873 Human RAB	c 789	11	100.0	5099	2	AAQ94445	Aaq94445 Bacterial
c 717	11	100.0	3872	2	AAZ39630	Aaz39630 Breast ca	c 790	11	100.0	5099	2	AAZ49503	Aaz49503 Transfer
c 718	11	100.0	3874	4	AAK71182	Aak71182 Human imm	c 791	11	100.0	5099	2	AAZ89159	Aaz89159 H. influe
c 719	11	100.0	3945	12	ADF72084	Adf72084 Mouse KPC	c 792	11	100.0	5099	2	AAV21431	Aav21431 H. influe
c 720	11	100.0	3964	4	ABR10590	Abi10590 Drosophil	c 793	11	100.0	5099	3	AAZ91001	Aaz91001 H. influe
c 721	11	100.0	3988	5	ABR17723	Abi17723 Human ner	c 794	11	100.0	5112	5	AAH81790	Aah81790 Human dif
c 722	11	100.0	4029	6	ABL69187	Abi69187 Prostate	c 795	11	100.0	5125	2	AAQ47196	Aaq47196 Plasmid p
c 723	11	100.0	4029	6	ABL69745	Abi69745 Prostate	c 796	11	100.0	5144	2	AAQ94446	Aaq94446 Bacterial
c 724	11	100.0	4029	6	ABN95785	Abn95785 Gene #228	c 797	11	100.0	5144	2	AAZ49504	Aaz49504 Transfer
c 725	11	100.0	4035	8	ABX34739	Abx34739 Human mdd	c 798	11	100.0	5144	2	AAZ89168	Aaz89168 H. influe
c 726	11	100.0	4044	2	AAQ85096	Aaq85096 Region up	c 799	11	100.0	5144	2	AAV21440	Aav21440 H. influe
c 727	11	100.0	4044	2	AAZ70214	Aaz70214 S. cyphim	c 800	11	100.0	5144	3	AAZ91002	Aaz91002 H. influe
c 728	11	100.0	4045	2	AAZ37251	Aaz37251 Human 3-O	c 801	11	100.0	5224	4	ABL25720	Abi25720 Drosophil
c 729	11	100.0	4054	4	ABL23578	Abi23578 Drosophil	c 802	11	100.0	5323	2	AAQ47195	Aaq47195 Plasmid p
c 730	11	100.0	4058	4	ABL03757	Abi03757 Drosophil	c 803	11	100.0	5379	8	ABT19761	Abt19761 Aspergill
c 731	11	100.0	4089	10	ADD14759	Adi14759 Human src	c 804	11	100.0	5397	4	ABL29757	Abi29757 Drosophil
c 732	11	100.0	4089	10	ADF81641	Adf81641 Leukaemia	c 805	11	100.0	5402	5	AAZ93666	Aaz93666 DNA encod
c 733	11	100.0	4089	13	ADR52786	Adr52786 Drug ther	c 806	11	100.0	5402	6	ABK83447	Abk83447 Human CDN
c 734	11	100.0	4119	4	AAH06664	Aah06664 Human rep	c 807	11	100.0	5402	8	ACC43649	Acc43649 Nucleotid
c 735	11	100.0	4119	4	AAH08003	Aah08003 Human ova	c 808	11	100.0	5402	8	AAZ50462	Aaz50462 KIAA0317
c 736	11	100.0	4132	6	ADP30558	Adp30558 Human kin	c 809	11	100.0	5402	10	ADF59746	Adf59746 Human con
c 737	11	100.0	4146	13	ADR14140	Adr14140 Human NF-	c 810	11	100.0	5403	12	ADO00893	Ado00893 Human hom
c 738	11	100.0	4202	5	ABR19239	Abi19239 Human ner	c 811	11	100.0	5403	12	ADO07699	Ado07699 Human pol
c 739	11	100.0	4214	4	ABL20859	Abi20859 Drosophil	c 812	11	100.0	5458	13	ADP54222	Adp54222 Human PRO
c 740	11	100.0	4214	5	ABV24766	Abv24766 Human pro	c 813	11	100.0	5475	10	ADF00552	Adf00552 Bacterial
c 741	11	100.0	4236	4	ABL07188	Abi07188 Drosophil	c 814	11	100.0	5513	6	ABN87479	Abn87479 Human dev
c 742	11	100.0	4254	5	ABX71276	Abx71276 Human bra	c 815	11	100.0	5533	12	ADO19175	Ado19175 Human PRO
c 743	11	100.0	4254	12	ADN05923	Adn05923 Antipsori	c 816	11	100.0	5544	2	AAV74421	Aav74421 Staphyloc
c 744	11	100.0	4259	4	ABL03078	Abi03078 Drosophil	c 817	11	100.0	5580	4	ABL12322	Abi12322 Drosophil
c 745	11	100.0	4290	10	ADF90750	Adf90750 Human hep	c 818	11	100.0	5637	13	ACN40745	Acn40745 Tumour-as
c 746	11	100.0	4292	10	ADF74205	Adf74205 Human nov	c 819	11	100.0	5640	13	ADP54397	Adp54397 Human PRO
c 747	11	100.0	4298	3	AZ48248	Aaz48248 Human oxi	c 820	11	100.0	5668	13	ADQ82885	Adq82885 Human KIA
c 748	11	100.0	4298	10	ADJ56287	Adj56287 Fruit fly	c 821	11	100.0	5760	8	ABX63067	Abx63067 Human CDN
c 749	11	100.0	4305	11	ADM86782	Adm86782 Human CDN	c 822	11	100.0	5762	6	AAZ94920	Aaz94920 Human DNA
c 750	11	100.0	4307	3	AAZ86947	Aaz86947 Inositolp	c 823	11	100.0	5762	6	ABS62765	Abs62765 Prostate

824	11	100.0	5816	6	ABQ61202	Abq61202 Human pro	897	11	100.0	9587	13	ADR82189	Adr82189 Hepatitis
825	11	100.0	5832	6	ABQ71069	Abq71069 listeria	898	11	100.0	9595	2	AAX24843	Aax24843 Infectiou
826	11	100.0	5918	6	ABL61773	Abi61773 Colon ade	899	11	100.0	9595	4	AAX23492	Aax23492 Infectiou
827	11	100.0	5918	6	ABN95264	Abn95264 Gene #176	900	11	100.0	9595	4	AAC86939	Aac86939 Nucleotid
828	11	100.0	5931	8	ACD05847	Acd05847 Novel hum	901	11	100.0	9595	12	ADO36222	Ado36222 Hepatitis
829	11	100.0	5961	4	AAL06666	Aal06666 Human rep	902	11	100.0	9595	12	ADO79396	Ado79396 Hepatitis
830	11	100.0	5961	4	ABR08005	Abra08005 Human ova	903	11	100.0	9599	2	AAX24833	Aax24833 Infectiou
C 831	11	100.0	6001	12	ADM47847	Adm47847 Polynucle	904	11	100.0	9599	2	AAX24832	Aax24832 Infectiou
C 832	11	100.0	6057	4	ABL06146	Abi06146 Drosophil	905	11	100.0	9599	4	AAX23491	Aax23491 Infectiou
C 833	11	100.0	6072	4	ABL13102	Abi13102 Drosophil	906	11	100.0	9599	4	AAC86938	Aac86938 Nucleotid
C 834	11	100.0	6156	2	AAV03517	Aav03517 Human tra	907	11	100.0	9599	12	ADJ56743	Adj56743 Hepatitis
C 835	11	100.0	6156	6	ABR98056	Abra98056 DNA encod	908	11	100.0	9599	12	ADJ64255	Adj64255 Hepatitis
C 836	11	100.0	6156	6	ABR935643	Abra935643 Human ste	909	11	100.0	9605	6	ABR91431	Abri91431 Hepatitis
C 837	11	100.0	6156	8	ABZ71960	Abz71960 Human cdn	910	11	100.0	9605	6	ABR91429	Abri91429 Hepatitis
C 838	11	100.0	6156	12	ADQ95897	Adq95897 T cell ac	911	11	100.0	9605	6	ABR91424	Abri91424 Hepatitis
C 839	11	100.0	6313	13	ADR25673	Adr25673 Breast ca	912	11	100.0	9605	6	ABR91432	Abri91432 Hepatitis
C 840	11	100.0	6314	10	ADL16199	Adl16199 Rat prote	913	11	100.0	9605	6	ABR91411	Abri91411 Hepatitis
C 841	11	100.0	6314	13	ADQ87404	Adq87404 Human tum	914	11	100.0	9605	6	ABR91430	Abri91430 Hepatitis
C 842	11	100.0	6349	4	ABL20858	Abi20858 Drosophil	915	11	100.0	9605	6	ABR91428	Abri91428 Hepatitis
C 843	11	100.0	6402	12	ADQ24795	Adq24795 Human sof	916	11	100.0	9605	6	ABR91425	Abri91425 Hepatitis
C 844	11	100.0	6417	12	ADN73990	Adn73990 Thale cre	917	11	100.0	9605	6	ABR91426	Abri91426 Hepatitis
C 845	11	100.0	6566	10	ADN09723	Adn09723 Novel DNA	918	11	100.0	9605	6	ABR91433	Abri91433 Hepatitis
C 846	11	100.0	6746	4	ABL03756	Abi03756 Drosophil	919	11	100.0	9605	6	ADN25332	Adn25332 Hepatitis
C 847	11	100.0	6807	13	ADR84342	Adr84342 Aspergill	920	11	100.0	9608	6	ABR91427	Abri91427 Hepatitis
C 848	11	100.0	7029	4	ABL29756	Abi29756 Drosophil	921	11	100.0	9622	10	AAI54424	Aai54424 Hepatitis
C 849	11	100.0	7106	2	AAQ47193	Aaq47193 Plasmid p	922	11	100.0	9646	6	ABR87285	Abri87285 CDNA enco
C 850	11	100.0	7106	2	AAQ97494	Aaq97494 pHCV167 s	923	11	100.0	9646	6	ABR87285	Abri87285 CDNA enco
C 851	11	100.0	7178	12	ADL72979	Adl72979 Hepatitis	924	11	100.0	9646	8	ACA62466	ACA62466 HCV H77 C
C 852	11	100.0	7298	2	AAQ47192	Aaq47192 Plasmid p	925	11	100.0	9652	4	ABL18818	Abi18818 Drosophil
C 853	11	100.0	7298	8	ADR41556	Adr41556 Human sec	926	11	100.0	9734	13	ACN41639	Acn41639 Human dia
C 854	11	100.0	7328	10	ADN33817	Adn33817 CDNA clon	927	11	100.0	9824	6	ABR51688	Abri51688 Human nuc
C 855	11	100.0	7328	10	ADA57687	Ada57687 BAC fragm	928	11	100.0	9824	9	ADB84030	Adb84030 Human NUR
C 856	11	100.0	7347	13	ADT05467	Adt05467 Haemophil	929	11	100.0	9824	9	ADB83988	Adb83988 Human NUR
C 857	11	100.0	7551	12	ADL72981	Adl72981 Hepatitis	930	11	100.0	9824	8	ABR655239	Abri655239 Human imm
C 858	11	100.0	7530	13	ADR84221	Adr84221 Aspergill	931	11	100.0	9872	8	ABZ73976	Abz73976 Secreted
C 859	11	100.0	7715	4	ABL21006	Abi21006 Drosophil	932	11	100.0	9872	10	ABT16916	Abt16916 Human sec
C 860	11	100.0	7754	12	ADL72977	Adl72977 Hepatitis	933	11	100.0	9872	10	ABZ67557	Abz67557 Human sec
C 861	11	100.0	7943	4	ABR83418	Abri83418 Human imm	934	11	100.0	9878	8	ABR65238	Abri65238 Human imm
C 862	11	100.0	8454	4	ABL24012	Abi24012 Drosophil	935	11	100.0	9878	8	ABZ73977	Abz73977 Secreted
C 863	11	100.0	8460	12	ADN11771	Adn11771 Hepatitis	936	11	100.0	9878	10	ABT16917	Abt16917 Human sec
C 864	11	100.0	8500	6	ABR93871	Abri93871 E. Coli/c	937	11	100.0	9878	10	ABZ67558	Abz67558 Human sec
C 865	11	100.0	8688	3	AAQ42748	Aaq42748 Arabidops	938	11	100.0	10061	13	ACN41638	Acn41638 Human dia
C 866	11	100.0	8688	6	ABZ13943	Abz13943 Arabidops	939	11	100.0	10231	5	ABA20864	Abi20864 Human ner
C 867	11	100.0	8730	4	AAK78558	Aak78558 Human imm	940	11	100.0	10231	8	ADA41555	Ada41555 Human sec
C 868	11	100.0	8730	4	AAK84610	Aak84610 Human imm	941	11	100.0	10231	10	ADD38116	Add38116 CDNA clon
C 869	11	100.0	8810	10	ABZ79879	Abz79879 Human nuc	942	11	100.0	10231	10	ADA57686	Ada57686 BAC fragm
C 870	11	100.0	9035	6	ABR89430	Abri89430 Human tum	943	11	100.0	10256	10	ADN63706	Adn63706 Human gen
C 871	11	100.0	9229	8	ABX34821	Abx34821 Human mdd	944	11	100.0	10256	10	ADN63702	Adn63702 Human gen
C 872	11	100.0	9365	6	AAQ25518	Aaq25518 Hepatitis	945	11	100.0	10256	10	ADN63714	Adn63714 Human gen
C 873	11	100.0	9370	2	AAQ75165	Aaq75165 AF-4 tran	946	11	100.0	10256	10	ADN63710	Adn63710 Human gen
C 874	11	100.0	9390	6	ABR83836	Abri83836 Human cdn	947	11	100.0	10803	10	ADD67945	Add67945 Modified
C 875	11	100.0	9390	9	ACF04208	Act04208 Human AF4	948	11	100.0	10803	10	ABX10617	Abx10617 MKO-Z nuc
C 876	11	100.0	9390	9	ACF04206	Act04206 Human AF4	949	11	100.0	10883	9	ADB84042	Adb84042 Human NUR
C 877	11	100.0	9390	10	ADN75439	Adn75439 Prostate	950	11	100.0	11042	4	ABL17026	Abi17026 Drosophil
C 878	11	100.0	9390	10	ADK67001	Adk67001 Gene #91	951	11	100.0	11062	6	AAI25331	Aai25331 Hepatitis
C 879	11	100.0	9390	12	ADQ87230	Adq87230 Human tum	952	11	100.0	11076	3	AAA98965	Aaa98965 Hepatitis
C 880	11	100.0	9390	13	ADR25359	Adr25359 Breast ca	953	11	100.0	11570	3	AAA95905	Aaa95905 Human KIX
C 881	11	100.0	9390	13	ADR66749	Adr66749 Human pro	954	11	100.0	11570	12	ADK52482	Adk52482 Human kal
C 882	11	100.0	9390	13	ADR66817	Adr66817 Human pro	955	11	100.0	11570	13	ADR72623	Adr72623 Human ren
C 883	11	100.0	9391	2	AAQ75164	Aaq75164 AF-4 tran	956	11	100.0	11570	13	ADR72875	Adr72875 Human ova
C 884	11	100.0	9401	2	AAI41882	Aai41882 Hepatitis	957	11	100.0	11674	3	AAX36210	Aax36210 Nucleotid
C 885	11	100.0	9402	2	AAQ41345	Aaq41345 Human hep	958	11	100.0	12119	4	AAC86936	Aac86936 Nucleotid
C 886	11	100.0	9405	2	AAQ40426	Aaq40426 Full-leng	959	11	100.0	12277	8	ABZ223912	Abz223912 Human 30S
C 887	11	100.0	9416	2	AAQ22871	Aaq22871 NANBV Hut	960	11	100.0	12413	4	ABL17040	Abi17040 Drosophil
C 888	11	100.0	9416	2	AAQ59378	Aaq59378 Hepatitis	961	11	100.0	12744	6	ABR78893	Abri78893 E. coli C
C 889	11	100.0	9416	6	ABR87300	Abri87300 CDNA enco	962	11	100.0	12744	10	ADH80460	Adh80460 Escherich
C 890	11	100.0	9416	8	ADN31764	Adn31764 Hepatitis	963	11	100.0	12822	4	ABL17012	Abi17012 Drosophil
C 891	11	100.0	9416	6	ACA62483	ACA62483 HCV-H cdn	964	11	100.0	12822	4	ABL02550	Abi02550 Drosophil
C 892	11	100.0	9416	5	AAQ03778	Aaq03778 Hepatitis	965	11	100.0	12980	2	AAV59364	Aav59364 Hepatitis
C 893	11	100.0	9518	5	AAQ03808	Aaq03808 Hepatitis	966	11	100.0	12980	6	ACA62466	ACA62466 DNA encod
C 894	11	100.0	9518	5	ABA19240	Abi19240 Human ner	967	11	100.0	13198	3	AAX36211	Aax36211 Nucleotid
C 895	11	100.0	9546	5	ABA19240	Abi19240 Human ner	968	11	100.0	13198	3	AAX36211	Aax36211 Nucleotid
C 896	11	100.0	9554	5	ABA19241	Abi19241 Human ner	969	11	100.0	13860	8	ACA44867	ACA44867 Prokaryot

c 970 11 100.0 13865 2 AAX13137  
 c 971 11 100.0 13865 6 ABS98932 Enterococ  
 c 972 11 100.0 14105 4 ABL29585  
 c 973 11 100.0 14707 6 AAL53529 Genomic D  
 c 974 11 100.0 15188 4 ABL25090 Drosophil  
 c 975 11 100.0 15565 4 AAK80612 Human imm  
 c 976 11 100.0 15613 4 AAL37160 Human mus  
 c 977 11 100.0 15613 8 ABX60148 cDNA enco  
 c 978 11 100.0 15613 12 ADJ30898 Human mus  
 c 979 11 100.0 16256 10 ADC86818 Human GPC  
 c 980 11 100.0 16256 3 AAZ36212 Nucleotid  
 c 981 11 100.0 16738 4 AAK70864 Human sof  
 c 982 11 100.0 17072 12 ADQ18719 Human sof  
 c 983 11 100.0 17212 4 ABL11550 Drosophil  
 c 984 11 100.0 17269 4 ABL29584 Drosophil  
 c 985 11 100.0 18564 4 AAK65368 Human imm  
 c 986 11 100.0 18564 8 ABZ74461 Secreted  
 c 987 11 100.0 18564 8 ADA98881 Human sec  
 c 988 11 100.0 19332 2 AAT46159 Cagi locu  
 c 989 11 100.0 21045 4 AAS26721 Human gen  
 c 990 11 100.0 21045 8 ABX74070 Human nov  
 c 991 11 100.0 21295 10 ADE54120 Human pro  
 c 992 11 100.0 22109 13 ABD33209 Murine ca  
 c 993 11 100.0 22419 11 ACN44908 Mouse gen  
 c 994 11 100.0 22874 4 ABL04654 Drosophil  
 c 995 11 100.0 23852 12 ADQ97840 Human can  
 c 996 11 100.0 25032 9 ADA02495 Mouse Myc  
 c 997 11 100.0 25032 10 ADB72233 Mouse Myc  
 c 998 11 100.0 25032 10 ADE82935 Mouse Myc  
 c 999 11 100.0 25032 10 ADE95743 Mouse myc  
 c1000 11 100.0 25772 4 AAK81332 Human imm

## ALIGNMENTS

RESULT 1  
 AAS02843/c  
 ID AAS02843 standard; DNA; 11 BP.  
 XX  
 AC AAS02843;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE Human pregnane X receptor (hPXR) gene, PCR primer #113.  
 XX  
 KW Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;  
 KW therapeutic; chemotherapy; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200120026-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 08-SEP-2000; 2000WO-EP008827.  
 XX  
 PR 10-SEP-1999; 99EP-00118120.  
 XX  
 PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
 XX  
 PI Wojnowski L, Hustert E;  
 XX  
 DR WPI; 2001-273428/28.  
 XX  
 PT Novel variant of the human pregnane X receptor gene, associated with  
 PT insufficient metabolism and/or sensitivity to drugs, is useful for  
 PT diagnosing and treating diseases with drugs that are modulators of their  
 PT gene product.  
 XX  
 PS Claim 1; Page 45; 108pp; English.  
 XX  
 CC AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding  
 sequences and PCR primers of the invention. The human pregnane X receptor  
 sequences are used to make antibodies, or a substance capable of binding  
 specifically to the gene product of hPXR gene, for diagnosing and  
 treating various diseases, such as cancer, with drugs that are  
 substrates, inhibitors or modulators of the hPXR gene product. The  
 proteins can be used to identify and obtain produgs and drugs for  
 treatment of diseases which are amenable to chemotherapy. The nucleic  
 acids can be used in gene therapy for the treatment or prevention of  
 disorders associated with hPXR expression

CC sequences and PCR primers of the invention. The human pregnane X receptor  
 sequences are used to make antibodies, or a substance capable of binding  
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 substrates, inhibitors or modulators of the hPXR gene product. The  
 proteins can be used to identify and obtain produgs and drugs for  
 treatment of diseases which are amenable to chemotherapy. The nucleic  
 acids can be used in gene therapy for the treatment or prevention of  
 disorders associated with hPXR expression  
 XX  
 SQ Sequence 11 BP; 4 A; 2 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 11; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CTTTGGCACTA 11  
 Db 11 CTTTGGCACTA 1  
 RESULT 2  
 AAS02842  
 ID AAS02842 standard; DNA; 11 BP.  
 XX  
 AC AAS02842;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE Human pregnane X receptor (hPXR) gene, PCR primer #112.  
 XX  
 KW Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;  
 KW therapeutic; chemotherapy; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200120026-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 08-SEP-2000; 2000WO-EP008827.  
 XX  
 PR 10-SEP-1999; 99EP-00118120.  
 XX  
 PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
 XX  
 PI Wojnowski L, Hustert E;  
 XX  
 DR WPI; 2001-273428/28.  
 XX  
 PT Novel variant of the human pregnane X receptor gene, associated with  
 PT insufficient metabolism and/or sensitivity to drugs, is useful for  
 PT diagnosing and treating diseases with drugs that are modulators of their  
 PT gene product.  
 XX  
 PS Claim 1; Page 45; 108pp; English.  
 XX  
 CC AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding  
 sequences and PCR primers of the invention. The human pregnane X receptor  
 sequences are used to make antibodies, or a substance capable of binding  
 specifically to the gene product of hPXR gene, for diagnosing and  
 treating various diseases, such as cancer, with drugs that are  
 substrates, inhibitors or modulators of the hPXR gene product. The  
 proteins can be used to identify and obtain produgs and drugs for  
 treatment of diseases which are amenable to chemotherapy. The nucleic  
 acids can be used in gene therapy for the treatment or prevention of  
 disorders associated with hPXR expression

Query Match 100.0%; Score 11; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

QY 1 CTTTGGCACTA 11  
 DB 1 CTTTGGCACTA 11

RESULT 3  
 ACD64825/c  
 ID ACD64825 standard; RNA; 17 BP.  
 XX  
 AC ACD64825;  
 XX  
 DT 30-SEP-2003 (first entry)  
 XX  
 DE HCV minus strand DNazyme substrate sequence #1736.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 306; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
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 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 5 A, 3 C, 7 G, 0 T; 2 U; 0 Other;  
 Query Match 100.0%; Score 11; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTGGCACTA 11  
 DB 17 CTTTGGCACTA 7

RESULT 4  
 ACD57843  
 ID ACD57843 standard; RNA; 17 BP.  
 XX  
 AC ACD57843;  
 XX  
 DT 23-SEP-2003 (first entry)  
 XX  
 DE HCV DNazyme substrate sequence #541.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 243; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention

XX Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 11; DB 8; Length 17;  
 Best Local Similarity 63.6%; Pred. No. 1.9e+03;  
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
 |::|||::|  
 Db 4 CUUUGGCACUA 14

RESULT 5  
 ACD57844

ID ACD57844 standard; RNA; 17 BP.

AC ACD57844;

DT 23-SEP-2003 (first entry)

DE HCV DNazyme substrate sequence #542.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyms; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

OS WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

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PA (LEEF/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;

XX

WIPI; 2003-229207/22.

Novel compound useful for treating cirrhosis, liver failure,  
 hepatocellular carcinoma, or condition associated with hepatitis C virus  
 infection.

Claim 1; Page 243; 387pp; English.

The present invention relates to nucleic acid molecules which modulate  
 the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
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 and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed  
 are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
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 as oligonucleotides that specifically bind the Enhancer I region of HBV  
 DNA. The nucleic acids may be used to modulate the expression of HBV  
 genes and HBV viral replication. Also disclosed is a method for screening  
 compounds and/or potential therapies directed against HBV, and compounds  
 that modulate the expression and/or replication of HCV. The compounds and  
 methods of the invention are useful for the treatment of degenerative and  
 disease states related to HBV and HCV infection, replication and gene  
 expression such as cirrhosis, liver failure, and hepatocellular  
 carcinoma. The present sequence represents a substrate for one of the HCV  
 DNazyme or minus strand DNazyme sequences disclosed in the present  
 invention

Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 11; DB 8; Length 17;

Best Local Similarity 63.6%; Pred. No. 1.9e+03;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

|::|||::|

Db 2 CUUUGGCACUA 12.

RESULT 6

ACD64826/c

ID ACD64826 standard; RNA; 17 BP.

AC ACD64826;

DT 30-SEP-2003 (first entry)

DE HCV minus strand DNazyme substrate sequence #1737.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyms; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.

XX WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.  
PA (MCSW/) MACEJACK D.  
PA (ROBE/) MCEWIGGEN J.  
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PA (PAVC/) PAVCO P.  
PA (LEEF/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Claim 1; Page 306; 387pp; English.  
XX  
CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
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CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
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CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
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CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNazyme or minus strand DNazyme sequences disclosed in the present  
CC invention  
XX  
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;  
Query Match 100.0%; Score 11; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. NO. 1.9e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTGGCACTA 11  
DB 15 CTTTGGCACTA 5  
RESULT 7  
ADI83295  
ID ADI83295 standard; RNA; 17 BP.  
XX  
AC ADI83295;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE HCV DNazyme substrate sequence #541.  
XX  
XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
KW HCV infection; type I interferon; DNazyme.  
XX  
XX Hepatitis C virus.  
OS  
XX US2003125270-A1.  
PN  
XX  
PD 03-JUL-2003.  
XX  
XX 18-DEC-2000; 2000US-00740332.  
PF  
XX 18-DEC-2000; 2000US-00740332.  
PR  
XX

PA (BLAT/) BLATT L.  
PA (MCSW/) MCEWIGGEN J.  
PA (ROBE/) ROBERTS E.  
PA (PAVC/) PAVCO P.A.  
PA (MACE/) MACEJACK D.  
XX  
PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;  
PI WPI; 2004-031273/03.  
XX  
XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
PT especially in combination with type I interferon therapy.  
XX  
XX Claim 1; SEQ ID NO 541; 198pp; English.  
XX  
CC The invention relates to an enzymatic nucleic acid molecule which  
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
CC the binding arms of the enzymatic nucleic acid molecule comprises  
CC sequences complementary to any of the defined substrate sequences given  
CC in the specification. The nucleic acid molecule may be administered for  
CC the treatment of HCV infections, especially in combination with type I  
CC interferons. The present sequence represents a HCV DNazyme substrate  
CC sequence.  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;  
Query Match 100.0%; Score 11; DB 12; Length 17;  
Best Local Similarity 63.6%; Pred. NO. 1.9e+03;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTGGCACTA 11  
DB 4 CUUUGGCACUA 14  
RESULT 8  
ADI86768/c  
ID ADI86768 standard; RNA; 17 BP.  
XX  
AC ADI86768;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE HCV DNazyme substrate sequence #4014.  
XX  
XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
KW HCV infection; type I interferon; DNazyme.  
XX  
XX Hepatitis C virus.  
OS  
XX US2003125270-A1.  
PN  
XX  
PD 03-JUL-2003.  
XX  
XX 18-DEC-2000; 2000US-00740332.  
PF  
XX 18-DEC-2000; 2000US-00740332.  
PR  
XX  
XX (BLAT/) BLATT L.  
PA (MCSW/) MCEWIGGEN J.  
PA (ROBE/) ROBERTS E.  
PA (PAVC/) PAVCO P.A.  
PA (MACE/) MACEJACK D.  
XX  
PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;  
PI WPI; 2004-031273/03.  
XX  
XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
PT especially in combination with type I interferon therapy.  
XX  
XX



```

PS Claim 1; SEQ ID NO 4014; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

Query Match          100.0%; Score 11; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB |||||
15 CTTTGGCACTA 5

RESULT 9
ADI86767/c
ID ADI86767 standard; RNA; 17 BP.
XX
AC ADI86767;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNazyme substrate sequence #4013.
XX
KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUL-2003.
XX
PF 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX
PN WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 4013; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 5 A; 3 C; 7 G; 0 T; 2 U; 0 Other;

Query Match          100.0%; Score 11; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB |||||
15 CTTTGGCACTA 5

RESULT 10
ADI83296
ID ADI83296 standard; RNA; 17 BP.
XX
AC ADI83296;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNazyme substrate sequence #542.
XX
KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUL-2003.
XX
PF 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX
PN WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 542; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;

Query Match          100.0%; Score 11; DB 12; Length 17;
Best Local Similarity 63.6%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB |||||
2 CUUUGGCACUA 12

RESULT 11
AAH23171
ID AAH23171 standard; DNA; 18 BP.
XX
AC AAH23171;
XX

```



DT 17-SEP-2001 (first entry)  
 XX Nitric oxide synthase gene nuclear factor 1 (NF-1) binding site.  
 DE  
 KW Hypertension; renal disease; non insulin dependent diabetes mellitus;  
 KW polymorphism; nitric oxide synthase; breast; lung; prostate; cancer;  
 KW nephrotropic; vasodilatory; renal injury; NIDDM; SNP; NOS; NF-1;  
 XX nuclear factor 1; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200153537-A2.  
 XX  
 XX 26-JUL-2001.  
 XX  
 XX 24-JAN-2001; 2001WO-US002260.  
 XX  
 PR 24-JAN-2000; 2000US-0177775P.  
 PR 25-JUL-2000; 2000US-0220662P.  
 XX  
 PA (DZGE-) DZ GENES LLC.  
 XX  
 PI Moskowitz DW;  
 XX  
 DR WPI; 2001-451916/48.  
 XX  
 XX The diagnosis of disorders, i.e. hypertension and non insulin dependent  
 PT diabetes mellitus comprises the identification of single polymorphism(s)  
 PT in a nitric oxide synthase gene.  
 XX  
 XX Example 4; Page 88; 119pp; English.  
 XX  
 CC The invention relates to diagnosing a genetic predisposition to disease,  
 CC condition or disorder i.e. hypertension, non insulin dependent diabetes  
 CC mellitus (NIDDM), end stage renal disease due to hypertension and/or  
 CC NIDDM mellitus that involves detecting the presence or absence of single  
 CC nucleotide polymorphisms (SNP) in the nitric oxide synthase gene (NOS).  
 CC The method is also useful for the treatment or prophylaxis of breast,  
 CC lung or prostate cancer. The method allows the identification of people  
 CC with a predisposition to disorders, before the disease progresses to an  
 CC end stage. The present sequence represents a nuclear factor 1 (NF-1)  
 CC binding site of the nitric oxide synthase gene, where a disruption occurs  
 CC due to a deletion polymorphism at position 1272 of the gene  
 XX  
 XX Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 11; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. NO. 1.9e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTGGCACTA 11  
 Db 1 CTTTGGCACTA 11  
 RESULT 12  
 AAX85553  
 ID AAX85553 standard; cDNA; 22 BP.  
 XX  
 AC AAX85553;  
 XX  
 XX 07-SEP-1999 (first entry)  
 DE PCR primer and probe used to detect human kin17 nucleic acids.  
 XX  
 KW Human; kin17 protein; cell proliferation; fertility; probe;  
 KW hyperproliferative disease; protein interaction; curved DNA;  
 KW HIV replication; HIV integration; repair enzyme; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN FR2772046-A1.

XX 11-JUN-1999.  
 PD  
 XX 09-DEC-1997; 97FR-00015536.  
 PF  
 XX 09-DEC-1997; 97FR-00015536.  
 PR  
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.  
 PA  
 XX Kannouche P, Mauffrey P, Pinon LG, Biard D, Angulo MJF;  
 PI  
 XX WPI; 1999-359999/31.  
 DR  
 XX New DNA coding for human kin17 protein - useful for controlling cell  
 PT proliferation or fertility.  
 PT  
 XX Claim 7; Page 5; 69pp; French.  
 PS  
 XX AAX85553-69 represent PCR primers and probes used to detect nucleic acids  
 CC encoding human kin17 protein. The mammalian kin17 protein is useful for  
 CC preparing a medicament for controlling cell proliferation or for  
 CC controlling fertility. The medicaments can also be used to treat  
 CC hyperproliferative diseases. Fragments between amino acids 55 and 235  
 CC (preferably between amino acids 129 and 228) of a mammalian kin17 protein  
 CC are useful for regulating the interaction between proteins and curved  
 CC DNA. The fragment can be used to block replication of HIV or its  
 CC integration into the human genome or to target repair enzymes to curved  
 CC DNA sites. Expression vectors for kin17 can be used for controlling cell  
 CC proliferation  
 XX  
 SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 11; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. NO. 1.9e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTGGCACTA 11  
 Db 12 CTTTGGCACTA 22  
 RESULT 13  
 AAX24199/c  
 ID AAX24199 standard; DNA; 23 BP.  
 XX  
 AC AAX24199;  
 XX  
 XX 11-SEP-2001 (first entry)  
 DT  
 XX PCR primer, SEQ ID NO:10, used to isolate ageing inhibition-related DNA.  
 DE  
 XX Mouse; ageing inhibition-related DNA; ageing inhibitory protein;  
 KW recombinant production; transgenic animal; detection; drug screening;  
 KW ligand identification; ageing-related disorder; premature ageing;  
 KW PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200138529-A1.  
 XX  
 XX 31-MAY-2001.  
 PD  
 XX 17-NOV-2000; 2000WO-JP008121.  
 PF  
 XX 19-NOV-1999; 99JP-00329649.  
 PR  
 XX (KYOW) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Shiraishi N, Sekine S, Nabeshima Y, Fujimori T, Ito S;  
 PI  
 XX WPI; 2001-367689/38.  
 DR  
 XX Polypeptide for treatment of premature aging.  
 PT

XX Example 1; Page 89; 94pp; Japanese.

PS The invention relates to 3 novel mouse proteins which inhibit ageing

XX (AAH73664-AAH73666) and to the nucleic acids encoding them (AAH24193-AAH24195). The invention also relates to recombinant vectors, host cells and transgenic non-human animals comprising DNA encoding a mouse ageing inhibitory protein of the invention; the recombinant production of a mouse ageing inhibitory protein; antibodies against the ageing inhibitory proteins; methods for immunologically assaying the proteins; and methods for identifying ligands or other modulators of the ageing inhibitory proteins, and the ligands and modulators thus identified. The ageing inhibitory proteins, nucleic acids encoding them, and antibodies, ligands and modulators, may be used in the diagnosis and treatment of ageing (particularly premature ageing), and ageing-related disorders. Sequences AAH24198-AAH24199 represent PCR primers used in an exemplification of the invention to isolate a mouse ageing inhibition-related DNA sequence (AAH24197)

XX Sequence 23 BP; 8 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 13 CTTTGGCACTA 3

RESULT 14

AAH76792

ID AAH76792 standard; DNA; 33 BP.

XX

AC AAH76792;

XX

14-DEC-2001 (first entry)

XX

Human bromo-domain 10 PCR primer, SEQ ID NO:6.

XX

Human; bromo-domain 10; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; inflammatory condition; cytostatic; anti-HIV; antiinflammatory; immunomodulator; PCR primer; ss.

XX

Homo sapiens.

XX

WO200172812-A1.

XX

04-OCT-2001.

XX

26-MAR-2001; 2001WO-CN000479.

XX

28-MAR-2000; 2000CN-00115196.

XX

(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX

Mao Y, Xie Y;

PI WPI; 2001-597108/67.

XX

Human bromo-domain 10 and encoded polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation.

XX

Example 4; Page 16; 32pp; Chinese.

XX

The invention relates to human bromo-domain 10 (AAG66746), nucleic acids encoding it (AAH76789), and a method for the recombinant production of bromo-domain 10. The protein has a molecular weight of 10 kD. The present invention additionally discloses an antagonist of bromo-domain 10 for therapeutic use, and an antibody which specifically binds to bromo-domain 10. Bromo-domain 10, and nucleotides which encode it may be used for

CC treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reactions or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences AAH76791-AAH76792 represent PCR primers used in an exemplification of the invention to amplify human bromo-domain 10 cDNA for cloning

XX Sequence 33 BP; 8 A; 10 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 5; Length 33;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||

Db 21 CTTTGGCACTA 31

RESULT 15

AAH38062/c

ID AAD38062 standard; DNA; 47 BP.

XX

AC AAD38062;

XX

10-SEP-2002 (first entry)

XX

Maize proRIP DNA amplifying PCR primer, RIP1BF.

XX

Maize; transgenic; transgenic plant; ribosome inactivating protein; RIP; cytotoxicity; nematode resistant plant; sterility; fruit abscission; viral infection; nematocide; antiviral; PCR; primer; ss.

XX

Zea mays.

OS

WO200233106-A2.

XX

25-APR-2002.

XX

15-OCT-2001; 2001WO-GB004581.

PF

14-OCT-2000; 2000GB-00025225.

PR

(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

PA

Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;

XX

WPI; 2002-454604/48.

XX

Producing transgenic plant resistant to nematode infection, comprises transforming plant with chimeric gene having promoter inducible at nematode feeding site, linked to sequence encoding maize ribosome inactivating protein.

XX

Example; Page 87; 89pp; English.

PS

The present invention relates to a novel method for producing transgenic plants which harbour chimeric genes within the genome of the plant, the expression of which gene causes plant cytotoxicity at a target site. The method involves transforming a plant with a chimeric gene comprising a promoter inducible at and/or adjacent to a target site, operably linked to a coding sequence encoding a maize ribosome inactivating protein (RIP) or its portion. The method is useful for producing transgenic plants harbouring within the genome a chimeric gene which when expressed, produces a cytotoxic protein. The target site may be a nematode feeding site and by targeting the nematode feeding site, nematode resistant plant can be obtained. If the target site is one or more of plant's pollen, anther or tapetum, the method is useful for effecting the male sterility in plants and if the target site is ovule of plant, the method is directed to effecting female sterility in plants. The target site may be specific parts of the flower or abscission zone of the leaf and/or fruit

CC and the method is useful for manipulating morphology of the flower of a  
CC plant and to assist in or promote leaf and/or fruit abscission in plants.  
CC The method is also useful for controlling viral infection. The present  
CC DNA sequence is a PCR primer which is used to amplify maize proRIP DNA.  
CC This primer is used in the exemplification of the invention

XX SQ Sequence 47 BP; 16 A; 9 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 40 CTTTGGCACTA 30

RESULT 16

AAI22229

ID AAI22229 standard; DNA; 77 BP.

XX AC

AAI22229;

DT 12-OCT-2001 (first entry)

DE Probe #12162 for gene expression analysis in human cervical cell sample.

XX Probe; human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer; ss.

XX Homo sapiens.

OS WO200157278-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000670.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488901/53.

DR Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human cervical epithelial cells.

XX Claim 25; SEQ ID NO 12162; 487pp; English.

CC The present invention relates to human single exon nucleic acid probes  
CC (SENPs). The present sequence is one such probe. The SENPs are derived  
CC from human HeLa cells. The SENPs can be used to produce a single exon  
CC microarray, which can be used for measuring human gene expression in a  
CC sample derived from human cervical epithelial cells. By measuring gene  
CC expression, the probes are therefore useful in grading and/or staging of  
CC diseases of the cervix, notably cervical cancer. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 11; DB 4; Length 77;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 34 CTTTGGCACTA 44

RESULT 17

ABA67308

ID ABA67308 standard; DNA; 77 BP.

XX AC

ABA67308;

DT 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #15613.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-483447/52.

DR Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human foetal liver.

XX Claim 4; SEQ ID NO 15613; 639pp + Sequence Listing; English.

CC The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human foetal liver. The  
CC present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 11; DB 4; Length 77;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11  
|||||  
Db 34 CTTTGGCACTA 44

RESULT 18

AAI47524

ID AAI47524 standard; DNA; 77 BP.

XX AC

AAI47524;

DT 17-OCT-2001 (first entry)

DE Probe #16210 used to measure gene expression in human placenta sample.  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KW Genetic disorder; ss.  
XX Homo sapiens.  
XX OS  
XX WO200157272-A2.  
PN  
XX  
PD 09-AUG-2001.  
XX  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488897/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
XX Claim 25; SEQ ID NO 16210; 654pp; English.  
XX  
XX The present invention relates to single exon nucleic acid probes (SENPs).  
CC The present sequence is one such probe. The probes are useful for  
CC producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders  
XX  
XX Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 11; DB 4; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CTTTGGCACTA 11  
DB 34 CTTTGGCACTA 44  
RESULT 19  
ABA49398  
ID ABA49398 standard; DNA; 77 BP.  
XX  
XX ABA49398;  
AC  
XX  
XX 01-FEB-2002 (first entry)  
DT  
XX  
XX Human breast cell single exon nucleic acid probe #8093.  
DE  
XX  
XX Human; microarray; single exon probe; gene expression; breast; disease;  
KW cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200157271-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000662.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR

PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-496933/54.  
XX  
XX New spatially-addressable set of single exon nucleic acid probes, useful  
PT for measuring gene expression in sample derived from human breast,  
PT comprises number of single exon nucleic acid probes.  
XX  
XX Claim 4; SEQ ID NO 8093; 327pp + Sequence Listing; English.  
XX  
XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and Br 474 cells. The method involves contacting the  
CC probes with a collection of detectably labelled nucleic acids derived  
CC from mRNA of human breast, and then measuring the label bound to each  
CC probe of the microarray. The probes are useful for verifying the  
CC expression of regions of genomic DNA predicted to encode proteins. They  
CC are useful for gene discovery, and for determining predisposition and/or  
CC prognosis breast disease. Gene expression analysis is useful for  
CC assessing the toxicity of chemical agents on cells. The microarray of  
CC this invention presents a far greater diversity of probes for measuring  
CC gene expression, with far less bias than expressed sequence tag  
CC microarrays. The method is suitable for rapid production of functional  
CC information from genomic sequence. The present sequence is a single exon  
CC nucleic acid probe of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;  
Query Match 100.0%; Score 11; DB 4; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CTTTGGCACTA 11  
DB 34 CTTTGGCACTA 44  
RESULT 20  
AAK41482  
ID AAK41482 standard; DNA; 77 BP.  
XX  
XX AAK41482;  
AC  
XX  
XX 06-NOV-2001 (first entry)  
DT  
XX  
XX Human bone marrow expressed single exon probe SEQ ID NO: 16039.  
DE  
XX  
XX Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200157276-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000668.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR

PR 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488900/53.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human bone marrow.  
XX Example 4; SEQ ID NO 16039; 658pp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
CC the probes of the invention  
XX  
SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;  
Query Match 100.0%; Score 11; DB 4; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTGGCACTA 11  
DB 34 CTTTGGCACTA 44  
RESULT 21  
AAK15744  
ID AAK15744 standard; DNA; 77 BP.  
XX  
AC AAK15744;  
XX  
XX 05-NOV-2001 (first entry)  
XX Human brain expressed single exon probe SEQ ID NO: 15735.  
XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
XX ss.  
XX Homo sapiens.  
XX WO200157275-A2.  
XX  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US000667.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483446/52.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX Example 4; SEQ ID NO 15735; 650pp + Sequence Listing; English.  
XX

CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention  
XX  
SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;  
Query Match 100.0%; Score 11; DB 4; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTGGCACTA 11  
DB 34 CTTTGGCACTA 44  
RESULT 22  
ABS41072  
ID ABS41072 standard; DNA; 77 BP.  
XX  
AC ABS41072;  
XX  
XX 25-FEB-2003 (first entry)  
XX Human liver single exon probe, SEQ ID NO 16062.  
XX Human; single exon nucleic acid probe; liver; cirrhosis;  
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
KW coronary heart disease; ss.  
XX Homo sapiens.  
XX WO200157273-A2.  
XX  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US000664.  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488998/53.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX Claim 4; SEQ ID NO 16062; 658pp; English.  
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
CC liver single exon nucleic acid probes of the invention. Note: The  
CC sequence information for this patent does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 77;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

|||||

DB 34 CTTTGGCACTA 44

RESULT 23

AAI07928  
ID AAI07928 standard; DNA; 77 BP.

XX

AC AAI07928;

XX

DT 09-OCT-2001 (first entry)

XX

DE Probe #7919 used to measure gene expression in human breast sample.

XX

KW Probe; human; breast disease; breast cancer; development disorder; ss;  
inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX

OS Homo sapiens.

XX

PN WO200157270-A2.

XX

PD 09-AUG-2001.

XX

PF 29-JAN-2001; 2001WO-US000661.

XX

PR 04-FEB-2000; 2000US-0180312P.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 30-JUN-2000; 2000US-00608408.

XX

PR 03-AUG-2000; 2000US-00632366.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX WPI; 2001-476286/51.

XX

DR Novel single exon nucleic acid probe used to measuring gene expression in  
a human breast.

XX

PT

XX

PS Claim 25; SEQ ID NO 7919; 322pp; English.

XX

CC The present invention relates to novel single exon nucleic acid probes.  
The present sequence is one such probe. The probes are useful for  
measuring human gene expression in a human breast sample, where the probe  
hybridises at high stringency to a nucleic acid expressed in the human  
breast. The probes are useful for predicting, diagnosing, grading,  
staging, monitoring and prognosing diseases of the human breast,  
particularly those diseases with polygenic aetiology. The diseases  
include: breast cancer, disorders of development, inflammatory diseases  
of the breast, fibrocystic changes, proliferative breast disease and non-  
carcinoma tumours. Note: The sequence data for this patent did not form  
part of the printed specification, but was obtained in electronic format  
directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 11; DB 5; Length 77;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

Db 34 CTTTGGCACTA 44

|||||

RESULT 24

ABS15487

ID ABS15487 standard; DNA; 77 BP.

XX

AC ABS15487;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human genome-derived single exon probe ORF from lung SEQ ID No 15478.

XX

KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
chronic obstructive pulmonary disease; interstitial lung disease;  
familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

KW Hermaneky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;

KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease; open reading frame; ORF.

XX

OS Homo sapiens.

XX

PN WO200186003-A2.

XX

PD 15-NOV-2001.

XX

PF 30-JAN-2001; 2001WO-US000665.

XX

PR 04-FEB-2000; 2000US-0180312P.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 30-JUN-2000; 2000US-00608408.

XX

PR 03-AUG-2000; 2000US-00632366.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX WPI; 2002-114183/15.

XX

PT Spatially-addressable set of single exon nucleic acid probes, used to  
measure gene expression in human lung samples.

XX

PS Claim 4; SEQ ID NO 15478; 634pp; English.

XX

CC The invention relates to a spatially-addressable set of single exon  
nucleic acid probes for measuring gene expression in a sample derived  
from human lung comprising single exon nucleic acid probes having one of  
12614 nucleic acid sequences mentioned in the specification, or their  
complements or the 12387 open reading frames derived from the 12614  
probes. Also included are a microarray comprising the novel set of probes  
; the novel set of probes which hybridise at high stringency to a nucleic  
acid expressed in the human lung; measuring gene expression in a sample  
derived from human lung, comprising (a) contacting the array with a  
collection of detectably labeled nucleic acids derived from human lung  
mRNA, and (b) measuring the label detectably bound to each probe of the  
array; identifying exons in a eukaryotic genome, comprising (a)  
algorithmically predicting at least one exon from genomic sequences of  
the eukaryote; and (b) detecting specific hybridisation of detectably  
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
in the above mentioned microarray; assigning exons to a single gene,  
comprising (a) identifying exons from genomic sequence by the method  
above and (b) measuring the expression of each of the exons in several  
tissues and/or cell types using hybridisation to a single exon of  
microarrays having a probe with the exon, where a common pattern of  
expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human  
CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a single exon probe open reading frame of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
DB 34 CTTTGGCACTA 44

## RESULT 25

AAC22084  
ID AAC22084 standard; cDNA; 100 BP.

XX AAC22084;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 26159.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
XX gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST ) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 26159; 71pp + Sequence Listing; English.

XX The present sequence is one of a large number of 5' ESTs derived from  
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively  
XX identified within the present sequence. The 5' ESTs were prepared from  
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
XX sequences usually correspond mainly to the 3' untranslated region (UTR)  
XX of the mRNA because they are often obtained from oligo-dT primed cDNA  
XX libraries. Such ESTs are not well suited for isolating cDNA sequences  
XX derived from the 5' ends of mRNAs and even in those cases where longer  
XX cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'  
XX ESTs are derived from mRNAs with intact 5' ends and can therefore be used

CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in  
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.  
CC They are used to obtain upstream regulatory sequences and to design  
CC expression and secretion vectors

XX SQ Sequence 100 BP; 32 A; 21 C; 14 G; 33 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 3; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
DB 81 CTTTGGCACTA 91

## RESULT 26

ABK26046/c

ID ABK26046 standard; DNA; 121 BP.

XX AC ABK26046;

XX 09-APR-2002 (first entry)

XX Amino acid overproduction genome altering oligonucleotide #118.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
XX o-methyl modification; LNA modification; phosphorothioate linkage;  
XX DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
XX abiotic stress tolerance; improved nutritional value; hygromycin-B;  
XX amino acid overproduction; herbicide resistance; glyphosate resistance;  
XX imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
XX porphyric herbicide resistance; triazine resistance; disease resistance;  
XX modified oil production; modified starch production; waxy starch;  
XX altered floral morphology; male-sterile plant; albino mutant;  
XX modified fatty acid content; reduced palmitate production; albino plant;  
XX increased stearate production; reduced linolenic acid production;  
XX photosynthetic process.

XX Oryza sativa.

XX Synthetic.

XX WO200192512-A2.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

XX 30-OCT-2000; 2000US-0244989P.

XX 27-MAR-2001; 2001US-00818875.

XX (UYDE ) UNIV DELAWARE.

XX Kmtec EB, Gamper HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful for  
XX creating plants with desired phenotypes, e.g. stress tolerance, improved  
XX nutritional value, herbicide or disease resistance, or modified oil  
XX production.

XX Claim 7; Page 128; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a  
XX genetic sequence, which comprises a single-stranded oligonucleotide  
XX having a DNA domain. The DNA domain has at least one mismatch with  
XX respect to the genetic sequence to be altered and further comprises  
XX chemical modifications of the oligonucleotide. The chemical modifications  
XX consist of o-methyl modification, an LNA modification, two or more  
XX phosphorothioate linkages on a terminus, or a combination of any two or  
XX more of these modifications. The oligonucleotides are useful for

CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention

XX SQ Sequence 121 BP; 28 A; 31 C; 24 G; 38 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
 |||||  
 Db 99 CTTTGGCACTA 89

# RESULT 27

ABK26045  
 ID ABK26045 standard; DNA; 121 BP.

XX AC ABK26045;

XX DT 09-APR-2002 (first entry)

XX DE Amino acid overproduction genome altering oligonucleotide #117.

XX KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KW o-methyl modification; LNA modification; phosphorothioate linkage;  
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW increased fatty acid content; reduced palmitate production; albino plant;  
 KW modified stearate production; reduced linolenic acid production;  
 KW photosynthetic process.

OS Oryza sativa.  
 OS Synthetic.

XX WO200192512-A2.

XX PD 06-DEC-2001.

XX PF 01-JUN-2001; 2001WO-US017672.

XX PR 01-JUN-2000; 2000US-0208538P.

XX PR 30-OCT-2000; 2000US-0244989P.

XX PR 27-MAR-2001; 2001US-00818875.

XX PA (UYDE ) UNIV DELAWARE.

XX PI Kmiec EB, Gamper HB, Rice MC, Kim J;

XX DR WPI; 2002-106307/14.

XX PT New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.

XX XX

PS Claim 7; Page 128; 220pp; English.

XX CC The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention

XX SQ Sequence 121 BP; 38 A; 24 C; 31 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
 |||||  
 Db 23 CTTTGGCACTA 33

# RESULT 28

ADN44736

ID ADN44736 standard; DNA; 121 BP.

XX AC ADN44736;

XX DT 15-JUL-2004 (first entry)

XX DE Mutant cell identification-related mutagenic oligonucleotide SeqID1405.  
 XX cell identification; oligonucleotide-directed sequence alteration;  
 KW selectable phenotype; transgenic plant; herbicide resistance;  
 KW sterile plant; abiotic stress tolerance; albino plant;  
 KW amino acid production; ss.

OS Oryza sativa.  
 OS Synthetic.

XX WO2004033708-A2.

XX PD 22-APR-2004.

XX PF 07-OCT-2003; 2003WO-US031862.

XX PR 07-OCT-2002; 2002US-0416983P.

XX PR 07-MAR-2003; 2003US-0453360P.

XX PA (UYDE ) UNIV DELAWARE.

XX PA (NAPR-) NAPRO BIO THERAPEUTICS INC.

XX PI Kmiec EB, Van Brabant A;

XX DR WPI; 2004-340941/31.

XX PT Identifying a cell with a desired oligonucleotide-directed sequence  
 PT alteration at a nucleic acid target site within the cell by identifying  
 PT the desired sequence alteration in cells selected for the presence of a



PT selectable phenotype.  
XX Example 27; SEQ ID NO 1405; 303pp; English.  
XX  
XX This invention relates to a novel method of identifying a cell having a  
CC desired oligonucleotide-directed sequence alteration at a first nucleic  
CC acid target site within the cell. The method comprises identifying the  
CC desired sequence alteration in cells that have been selected for the  
CC presence of a selectable phenotype conferred by a concurrent  
CC oligonucleotide-directed sequence alteration at a second nucleic acid  
CC target site within the cells. The method is useful in identifying a cell  
CC having a desired oligonucleotide-directed sequence alteration at a first  
CC nucleic acid target site within the cell. The method may be useful for  
CC the production of plants with herbicide resistance, male or female  
CC sterile plants, abiotic stress tolerance, albino plants or plants with  
CC altered amino acid production as well as for use in mammalian cell lines.  
CC The present sequence is that of a mutagenic oligonucleotide which was  
CC used in the exemplification of the invention.  
XX  
SQ Sequence 121 BP; 38 A; 24 C; 31 G; 28 T; 0 U; 0 Other;  
Query Match 100.0%; Score 11; DB 12; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CTTTGGCACTA 11  
DB 23 CTTTGGCACTA 33  
RESULT 29  
ADN44737/c  
ID ADN44737 standard; DNA; 121 BP.  
AC ADN44737;  
XX  
XX 15-JUL-2004 (first entry)  
DE Mutant cell identification-related mutagenic oligonucleotide SeqID1406.  
XX cell identification; oligonucleotide-directed sequence alteration;  
KW selectable phenotype; transgenic plant; herbicide resistance;  
KW sterile plant; abiotic stress tolerance; albino plant;  
KW amino acid production; ss.  
XX  
XX Oryza sativa.  
OS Synthetic.  
XX  
XX WO2004033708-A2.  
PN  
XX  
XX 22-APR-2004.  
PD  
XX  
XX 07-OCT-2003; 2003WO-US031862.  
PF  
XX  
XX 07-OCT-2002; 2002US-0416983P.  
PR  
XX  
XX 07-MAR-2003; 2003US-0453360P.  
PR  
XX  
XX (UYDE ) UNIV DELAWARE.  
PA (NAPRO-) NAPRO BIO THERAPEUTICS INC.  
XX  
XX Kmiec BB, Van Brabant A;  
PI  
XX  
XX WPI; 2004-340941/31.  
DR  
XX  
XX Identifying a cell with a desired oligonucleotide-directed sequence  
PT alteration at a nucleic acid target site within the cell by identifying  
PT the desired sequence alteration in cells selected for the presence of a  
PT selectable phenotype.  
XX  
XX Example 27; SEQ ID NO 1406; 303pp; English.  
PS  
XX This invention relates to a novel method of identifying a cell having a  
CC desired oligonucleotide-directed sequence alteration at a first nucleic  
CC acid target site within the cell. The method comprises identifying the  
CC desired sequence alteration in cells that have been selected for the  
CC presence of a selectable phenotype conferred by a concurrent  
CC oligonucleotide-directed sequence alteration at a second nucleic acid  
CC target site within the cells. The method is useful in identifying a cell  
CC having a desired oligonucleotide-directed sequence alteration at a first  
CC nucleic acid target site within the cell. The method may be useful for  
CC the production of plants with herbicide resistance, male or female  
CC sterile plants, abiotic stress tolerance, albino plants or plants with  
CC altered amino acid production as well as for use in mammalian cell lines.  
CC The present sequence is that of a mutagenic oligonucleotide which was  
CC used in the exemplification of the invention.  
XX  
SQ Sequence 121 BP; 38 A; 24 C; 31 G; 28 T; 0 U; 0 Other;  
Query Match 100.0%; Score 11; DB 12; Length 121;  
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CTTTGGCACTA 11  
DB 99 CTTTGGCACTA 89  
RESULT 30  
AAI23415/c  
ID AAI23415 standard; DNA; 153 BP.  
XX  
XX  
AC AAI23415;  
XX  
XX 12-OCT-2001 (first entry)  
DT  
XX  
XX Probe #13348 for gene expression analysis in human cervical cell sample.  
DE  
XX Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200157278-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000670.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX 30-JUN-2000; 2000US-00608408.  
PR  
XX 03-AUG-2000; 2000US-00632366.  
PR  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX 04-OCT-2000; 2000GB-00024263.  
PR  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-489501/53.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human cervical epithelial cells.  
PT  
XX Claim 25; SEQ ID NO 13348; 487pp; English.  
PS  
XX The present invention relates to human single exon nucleic acid probes  
CC (SENPs). The present sequence is one such probe. The SENPs are derived  
CC from human HeLa cells. The SENPs can be used to produce a single exon  
CC microarray, which can be used for measuring human gene expression in a  
CC sample derived from human cervical epithelial cells. By measuring gene  
CC expression, the probes are therefore useful in grading and/or staging of  
CC diseases of the cervix, notably cervical cancer. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at



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PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
XX PT for measuring gene expression in sample derived from human breast,
XX PT comprises number of single exon nucleic acid probes.
XX
XX Claim 4; SEQ ID NO 9260; 327bp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting the
XX probes with a collection of detectably labelled nucleic acids derived
XX from mRNA of human breast, and then measuring the label bound to each
XX probe of the microarray. The probes are useful for verifying the
XX expression of regions of genomic DNA predicted to encode proteins. They
XX are useful for gene discovery, and for determining predisposition and/or
XX prognosing breast disease. Gene expression analysis is useful for
XX assessing the toxicity of chemical agents on cells. The microarray of
XX this invention presents a far greater diversity of probes for measuring
XX gene expression, with far less bias than expressed sequence tag
XX microarrays. The method is suitable for rapid production of functional
XX information from genomic sequence. The present sequence is a single exon
XX nucleic acid probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB |||||
99 CTTTGGCACTA 89

RESULT 34
ABA35504/c
ID ABA35504 standard; DNA; 153 BP.
XX
XX AC ABA35504;
XX
XX DT 23-JAN-2002 (first entry)
XX
XX DE Probe #13970 for gene expression analysis in human heart cell sample.
XX
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200157274-A2.
XX
XX PD 09-AUG-2001.

PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX
XX Claim 4; SEQ ID NO 13970; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB |||||
99 CTTTGGCACTA 89

RESULT 35
AAK42661/c
ID AAK42661 standard; DNA; 153 BP.
XX
XX AC AAK42661;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 17218.
XX
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200157276-A2.
XX
XX PD 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
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XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX Example 4; SEQ ID NO 17218; 658pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX the probes of the invention
XX
XX Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 11; DB 4; Length 153;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+03;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CTTTGGCACTA 11
XX Db 99 CTTTGGCACTA 89
XX
XX RESULT 36
XX AAK16890/c
XX ID AAK16890 standard; DNA; 153 BP.
XX AC AAK16890;
XX XX
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 16881.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX Example 4; SEQ ID NO 16881; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention
XX
XX Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 11; DB 4; Length 153;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+03;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CTTTGGCACTA 11
XX Db 99 CTTTGGCACTA 89
XX
XX RESULT 37
XX ABS42283/c
XX ID ABS42283 standard; DNA; 153 BP.
XX AC ABS42283;
XX XX
XX DT 25-FEB-2003 (first entry)
XX DE Human liver single exon probe, SEQ ID NO 17273.
XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
XX KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX KW coronary heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX Claim 4; SEQ ID NO 17273; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABS25011-ABS51005 represent human
XX liver single exon nucleic acid probes of the invention. Note: The
XX sequence information for this patent does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
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```
SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;
Query Match      100.0%; Score 11; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
Db      99 CTTTGGCACTA 89

RESULT 38
AAI09041/c
ID AAI09041 standard; DNA; 153 BP.
XX
AC AAI09041;
XX
DT 09-OCT-2001 (first entry)
XX
DE Probe #9032 used to measure gene expression in human breast sample.
XX
KW Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US000661.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-0060840B.
PR 03-AUG-2000; 2000US-0063236F.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
XX
PS Claim 25; SEQ ID NO 9032; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes.
CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridises at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and non-
CC carcinoma tumours. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pt_sequences
XX
SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;
Query Match      100.0%; Score 11; DB 5; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
Db      99 CTTTGGCACTA 89

RESULT 39
ABS16713/c
ID ABS16713 standard; DNA; 153 BP.
XX
AC ABS16713;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 16704.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX Homo sapiens.
OS
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-0060840B.
XX 03-AUG-2000; 2000US-0063236F.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 16704; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
```

CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hexmanský-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagazer syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe open reading frame of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
 |||||  
 Db 99 CTTTGGCACTA 89

## RESULT 40

ACF72987/C  
 ID ACF72987 standard; DNA; 204 BP.

XX AC ACF72987;

XX DT 20-NOV-2003 (first entry)

XX DE Staphylococcus aureus DNA #667.

XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;  
 KW enzymatic assay; antibiotic target; gene; ds.

XX OS Staphylococcus aureus.

XX PN WO200294868-A2.

XX PD 28-NOV-2002.

XX PF 27-MAR-2002; 2002WO-IB002637.

XX PR 27-MAR-2001; 2001GB-00007661.

XX PA (CHIR-) CHIRON SPA.

XX PI Masignani V, Mora M, Scarselli M;

XX DR WPI; 2003-120786/11.

XX DR P-PSDB; ABW71427.

XX PT New Staphylococcus aureus protein, useful as a vaccine for treating or  
 PT preventing Staphylococcal infection, specifically an infection caused by  
 PT S. aureus, e.g. sepsis.

XX PS Claim 6; SEQ ID NO 1333; 49pp; English.

XX CC The invention relates to novel genes and encoded proteins from  
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a  
 CC nucleic acid encoding the protein, or an antibody to the protein, is  
 CC useful as a pharmaceutical, particularly as a vaccine for treating or  
 CC preventing infection due to Staphylococcus bacteria, specifically an  
 CC infection caused by S. aureus. The composition is particularly useful for  
 CC treating or preventing sepsis in a patient. The composition can also be  
 CC used for diagnostics. The protein is also used in an assay for enzymatic  
 CC studies and as a target for antibiotics. This sequence represents one of  
 CC the novel S. aureus genes of the invention

XX

SQ Sequence 204 BP; 76 A; 30 C; 35 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 8; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
 |||||  
 Db 109 CTTTGGCACTA 99

## RESULT 41

ABS68966  
 ID ABS68966 standard; DNA; 213 BP.

XX AC ABS68966;

XX DT 21-NOV-2002 (first entry)

XX DE Novel murine polynucleotide isolated using gene trap technology #29.

XX KW Mouse; gene trapped sequence; GTS; functional genomic analysis;  
 KW phage display system; gene chip; temporal gene expression;  
 KW tissue specific gene expression; antisense inhibition; gene targeting;  
 KW development disorder; cell differentiation disorder; aging; cancer;  
 KW autoimmune disease; lupus; inflammatory disorder; skin disorder;  
 KW degenerative disorder; ds.

XX OS Mus musculus.

XX PN US2002102543-A1.

XX PD 01-AUG-2002.

XX PF 30-NOV-2000; 2000US-00728445.

XX PR 01-DEC-1999; 99US-0168358P.

XX PA (FRIE/) FRIEDRICH G.

XX PA (ZAMB/) ZAMBROWICZ B.

XX PA (SAND/) SANDS A T.

XX PI Friedrich G, Zambrowicz B, Sands AT;

XX DR WPI; 2002-690598/74.

XX PT Novel murine polynucleotides that individually identify novel genes into  
 PT which a retroviral gene trap vector has integrated, useful in genomic  
 PT analysis and in discovery, development of therapeutic and diagnostic  
 PT agents.

XX PS Claim 1; Page 35; 296pp; English.

XX CC The invention describes an isolated murine polynucleotide (I) comprising  
 CC a contiguous stretch of at least 60 nucleotides of one of 265-677  
 CC nucleotide 891 OMNIBANK gene trapped sequences (GTSs) (S), given in the  
 CC specification. The novel genes and cells are useful in functional genomic  
 CC analysis and in the discovery and development of new therapeutic and  
 CC diagnostic agents and methods. (I) is useful for identifying the coding  
 CC regions of the murine genome, to isolate cDNAs, genomic clones, or full-  
 CC length genes/polynucleotides or homologues, heterologues, paralogues, or  
 CC orthologues that are capable of hybridising to one or more of the GTSs  
 CC under stringent conditions. (I) can be incorporated into a phage display  
 CC system that can be used to screen for proteins, or other ligands, that  
 CC are capable of binding an amino acid sequence encoded by an  
 CC oligonucleotide or polynucleotide sequence in at least one of the TS  
 CC sequences. (I) is useful in addressable arrays, such as gene chips, to  
 CC identify and characterise temporal and tissue specific gene expression,  
 CC to identify the gene of interest from many sources and for genetic  
 CC manipulations such as antisense inhibition and gene targeting. Decreasing  
 CC the level of expression of (I) and/or down regulating the activity of  
 CC peptides or proteins encoded by (I) is useful for treating development  
 CC and cell differentiation disorders, aging, cancer, autoimmune disease,

CC lupus, inflammatory disorders, skin disorders and degenerative disorders.  
CC This sequence represents a murine cDNA isolated using gene trap  
CC technology

SQ Sequence 213 BP; 53 A; 37 C; 36 G; 87 T; 0 U; 0 Other;  
Query Match 100.0%; Score 11; DB 6; Length 213;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCACTA 11  
|||||  
Db 175 CTTGGCACTA 185

RESULT 42  
ABL71901/c  
ID ABL71901 standard; cDNA; 240 BP.

XX ABL71901;

XX 14-MAY-2002 (first entry)

DE Corn tassell-derived polynucleotide (cdps) SEQ ID NO:1275.

XX Corn; corn tassell-derived polynucleotide; cdps; hybrid breeding; CDps;  
KW inheritance; characteristic; growth; development; disease resistance;  
KW environmental adaptability; quality; yield; molecular marker;  
KW multigene trait; plant breeding; corn tassell; gene; ss.

XX Zea mays.

OS US2001051335-A1.

PN 13-DEC-2001.

PD 16-APR-1999; 99US-00294093.

PF 21-APR-1998; 98US-0082567P.

PR (LALG/) LALGUDI R V.

PA (ITOL/) ITO L Y.

PA (SHER/) SHERMAN B K.

XX Lalgudi RV, Ito LY, Sherman BK;

XX WPI; 2002-163647/21.

XX Novel purified corn tassell-derived polynucleotide useful for determining  
PT altered gene expression, to recover regulatory elements and to follow  
PT inheritance of desirable characteristics through hybrid breeding  
PT programs.

XX Claim 1; SEQ ID NO 1275; 201pp; English.

XX The present sequence describes a purified corn tassell-derived  
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence  
CC selected from those given in ABL70627 to ABL76833. The cdps sequences  
CC encode corn tassell-derived polypeptides (CDPs). The cdps sequences (I)  
CC can be used for determining altered gene expression, to recover  
CC regulatory elements and to follow inheritance of desirable  
CC characteristics through hybrid breeding programs. (I) are also useful in  
CC the evaluation, and alteration of desired characteristics associated with  
CC growth and development, disease resistance, environmental adaptability,  
CC quality and yield, and as molecular markers for studying inheritance of  
CC multigene traits in a plant breeding program. (I) can be used to produce  
CC a tassell-specific profile of gene transcription, a transcript image, to  
CC clone regulatory elements for use in transformation vectors, to express a  
CC polypeptide, to identify, isolate or extend identical or related corn  
CC tassell nucleic acid sequences from DNA libraries, in nucleic acid  
CC hybridisation or amplification technologies, as query sequences to  
CC determine homology of known sequences, as probe for use in Southern or  
CC Northern hybridisation, and to identify the presence of and/or to

CC determine the degree of similarity between two (or more) nucleic acid  
CC sequences

SQ Sequence 240 BP; 79 A; 68 C; 49 G; 44 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 240;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCACTA 11  
|||||  
Db 120 CTTGGCACTA 110

RESULT 43

ABAL1368

ID ABAL1368 standard; cDNA; 245 BP.

XX ABAL1368;

XX 23-JAN-2002 (first entry)

DE Human nervous system related polynucleotide SEQ ID NO 375.

XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;  
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; antitumor; antitumor;  
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.

OS Homo sapiens.

XX WO200159063-A2.

XX 16-AUG-2001.

XX 17-JAN-2001; 2001WO-US001334.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0217496P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0233397P.  
 PR 14-SEP-2000; 2000US-0233398P.  
 PR 14-SEP-2000; 2000US-0233399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 25-SEP-2000; 2000US-0234998P.  
 PR 26-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 27-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 13-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 20-OCT-2000; 2000US-0241826P.  
 PR 20-OCT-2000; 2000US-0242221P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 01-DEC-2000; 2000US-0251160P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251859P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-541565/60.

DR P-PSDB; ABB15042.

XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating nervous system cancers  
 PT and metastases.

XX Claim 1; SEQ ID NO 375; 1701pp + Sequence Listing; English.

XX The invention relates to novel genes (ABA11004-ABA21534) and proteins  
 CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 245 BP; 35 A; 66 C; 82 G; 60 T; 0 U; 2 Other;

Query Match 100.0%; Score 11; DB 5; Length 245;  
 Best Local Similarity 100.0%; Pred. NO. 2.1e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTGGGCACTA 11

DB 107 CTTTGGGCACTA 117



```
RESULT 44
ABN24053/c
ID ABN24053 standard; cDNA; 246 BP.
XX
AC ABN24053;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human ORFX polynucleotide sequence SEQ ID NO:16583.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US010836.
XX
PR 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach MD;
XX
DR WPI; 2002-106308/14.
DR P-PSDB; ABP08301.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
XX
PS Disclosure; SEQ ID NO 16583; 1037pp; English.
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP0010 to ABP1500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 246 BP; 85 A; 31 C; 53 G; 72 T; 0 U; 5 Other;

Query Match 100.0%; Score 11; DB 6; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 45
AAH81973/c
ID AAH81973 standard; DNA; 255 BP.
XX
AC AAH81973;
XX
DT 21-SEP-2001 (first entry)
XX
DE Rat differential transcription-associated cDNA SEQ ID 482.
XX
KW Differential transcription; human; rat; tumour cell; cytostatic;
KW Ras modulator; Class II tumour suppressor gene; gene therapy; ss.
XX
OS Rattus sp.
XX
PN WO200157058-A2.
XX
PD 09-AUG-2001.
XX
PF 31-JAN-2001; 2001WO-EP001003.
XX
PR 31-JAN-2000; 2000DE-01004102.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Hinzmann B, Schaefer R, Zuber J, Tchernitsa O;
PI Grips M, Hellriegel M, Schmitz A, Sers C;
XX
DR WPI; 2001-483415/52.
XX
PT Nucleic acids differentially expressed between tumor and normal cells,
PT useful for diagnosis or therapy of tumors and for screening active
PT agents.
XX
PS Claim 6; Page 505; 579pp; German.
XX
CC This invention describes a nucleic acid (I) with differential expression
CC between tumour and normal cells and which has cytostatic activity. (I)
CC work as modulators of Ras activity by inducing expression of tumour
CC suppressor genes. (I), and polypeptides encoded by them, are useful as
CC targets for diagnosis or therapy and in screening to determine the
CC effects of an active compound (potential pharmaceutical) on a cell line,
CC particularly for diagnosis and treatment of tumors, especially by
CC modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
CC methods) or by modulating the amount and/or location of (I)-encoded
CC polypeptides (by administration of the polypeptide or its activator,
CC antibody (optionally as a conjugate) or inhibitor). The method allows
CC identification of many Class II tumour suppressor genes (i.e. genes that
CC are not primary targets for tumour-initiating mutations). AAH81492-
CC AAH82376 represent the human and rat derived nucleic acid fragments
CC described in the method of the invention
XX
SQ Sequence 255 BP; 73 A; 66 C; 51 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 5; Length 255;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB 24 CTTTGGCACTA 14

RESULT 46
ADS68954
ID ADS68954 standard; cDNA; 256 BP.
XX
QY 1 CTTTGGCACTA 11
DB 247 CTTTGGCACTA 237
```

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AC ADS68954;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Corn seedling-derived polynucleotide (cpds), SEQ ID 3970.
XX
XX DE Corn, seedling-derived polynucleotide; cdp; ss; plant; seed growth;
XX seed development; disease resistance; insect infestation; fungal disease;
XX bacterial infection; Goss' Bacterial Wilt; blight;
XX Stewart's bacterial wilt; Holcus spot; bacterial leaf blight; leaf spot;
XX bacterial stripe; maize dwarf mosaic virus infection;
XX environmental stress; water stress; pH stress; temperature stress;
XX pollution; injury; pesticide.
XX
XX OS Zea mays.
XX
XX PN US2003237110-A9.
XX
XX PD 25-DEC-2003.
XX
XX PF 06-AUG-2001; 2001US-00923876.
XX
XX PR 12-MAY-1998; 98US-0085331P.
XX
XX PR 21-APR-1999; 99US-00298329.
XX
XX PA (INCY-) INCYTE PHARM INC.
XX
XX PI Lalgudi RV, Ito LY, Sherman BK;
XX
XX DR WPI; 2002-195165/25.
XX
XX PT New corn seedling-derived polynucleotides and polypeptides, useful in
XX identifying and altering desired characteristics associated with growth
XX and development, disease resistance, environmental adaptability, quality
XX and yield.
XX
XX PS Claim 1; SEQ ID NO 3970; 33pp; English.
XX
XX CC The invention relates to a corn seedling-derived polynucleotide (cdp)
XX selected from ADS64985-ADS71316, or their complements and fragments. Also
XX included are a composition for the detection of altered expression of a
XX cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a
XX method of detecting a polynucleotide in a biological sample using a cdp,
XX a method for using oligomers (and amplification) to recover a regulatory
XX element from a DNA library using oligomers designed against a cdp, a
XX seedling specific regulatory element that regulates the expression of a
XX cdp, an expression vector containing a cdp or regulatory element, a plant
XX transformed with the vector, a host cell containing the vector (and
XX expressing a corn seedling derived protein, CDP), an anti-CDP antibody,
XX identifying a compound which binds a CDP and screening a plurality of
XX compounds for binding to cdp polynucleotide. The cdp polynucleotides,
XX proteins, vectors, cells and antibodies are useful for the
XX identification, evaluation and alteration of seed growth and development,
XX disease resistance (e.g. to insect infestation, fungal disease, bacterial
XX infection, Goss' Bacterial Wilt, blight, Stewart's bacterial wilt, Holcus
XX spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
XX mosaic virus infection) and resistance to environmental stress (e.g.
XX water stress, pH stress, temperature stress, pollution, injury or
XX pesticides. The present sequence is cdp cDNA sequence.
XX
XX SQ Sequence 256 BP; 77 A; 57 C; 55 G; 65 T; 0 U; 2 Other;

Query Match 100.0%; Score 11; DB 7; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB 65 CTTTGGCACTA 75

RESULT 47
ABQ67322/c
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ID ABQ67322 standard; DNA; 273 BP.
XX
XX AC ABQ67322;
XX
XX DT 29-AUG-2002 (first entry)
XX
XX DE Listeria innocua DNA sequence #124.
XX
XX KW Antibacterial; Listeria; food contamination; mutational analysis;
XX infection; ds.
XX
XX OS Listeria innocua.
XX
XX PN WO200228891-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 04-OCT-2001; 2001WO-FR003061.
XX
XX PR 04-OCT-2000; 2000FR-00012697.
XX
XX PA (INSP ) INST PASTEUR.
XX
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX PI Kunst F, Glaser P;
XX
XX DR WPI; 2002-332479/37.
XX
XX PT New genomic sequences from Listeria species, useful for detection,
XX treatment and prevention of infection, also related polypeptides,
XX antibodies and modulators.
XX
XX PS Claim 7; SEQ ID NO 135; 180pp; French.
XX
XX CC The present invention relates to nucleic acid sequences (ABQ67188-
XX ABQ71212) from Listeria sp. The sequences are useful as probes and
XX primers for identification and/or detection of Listeria (e.g. as
XX contaminants in foods, or mutational analysis) and for analysis of gene
XX expression. Proteins encoded by the nucleic acid sequences can be used to
XX screen for compounds that modulate gene expression, replication and
XX pathogenicity of Listeria (potential therapeutic agents), also for
XX treating infections by Listeria, and are useful as immunogens in anti-
XX Listeria vaccines. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 273 BP; 90 A; 53 C; 39 G; 91 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB 85 CTTTGGCACTA 75

RESULT 48
AAC23036
ID AAC23036 standard; cDNA; 276 BP.
XX
XX AC AAC23036;
XX
XX DT 06-OCT-2000 (first entry)
XX
XX DE Human secreted protein 5' EST, SEQ ID NO: 27111.
XX
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1033401-A2.
```

XX 06-SEP-2000.  
 XX  
 XX 21-FEB-2000; 2000EP-00200610.  
 XX  
 XX 26-FEB-1999; 99US-0122487P.  
 XX  
 XX (GEST ) GENSET.  
 XX  
 XX Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 XX WPI; 2000-500381/45.  
 XX  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 XX diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 XX  
 XX Claim 1; SEQ.ID NO 27111; 71pp + Sequence Listing; English.  
 XX  
 XX The present sequence is one of a large number of 5' ESTs derived from  
 XX mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 XX identified within the present sequence. The 5' ESTs were prepared from  
 XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 XX sequences usually correspond mainly to the 3' untranslated region (UTR)  
 XX of the mRNA because they are often obtained from oligo-dT primed cDNA  
 XX libraries. Such ESTs are not well suited for isolating cDNA sequences  
 XX derived from the 5' ends of mRNAs and even in those cases where longer  
 XX cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'  
 XX ESTs are derived from mRNAs with intact 5' ends and can therefore be used  
 XX to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in  
 XX diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 XX They are used to obtain upstream regulatory sequences and to design  
 XX expression and secretion vectors  
 XX  
 XX Sequence 276 BP; 100 A; 49 C; 48 G; 77 T; 0 U; 2 Other;  
 XX  
 XX Query Match 100.0%; Score 11; DB 3; Length 276;  
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 CTTTGGCACTA 11  
 XX |||||  
 XX Db 219 CTTTGGCACTA 229  
 XX  
 XX RESULT 49  
 XX AAL23068  
 XX ID AAL23068 standard; cDNA; 284 BP.  
 XX AC  
 XX AAL23068;  
 XX  
 XX 07-DEC-2001 (first entry)  
 XX  
 XX DE Human breast cancer expressed polynucleotide 15525.  
 XX  
 XX KW Human; breast cancer; cell marker; cytostatic; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX WO200151628-A2.  
 XX  
 XX PD 19-JUL-2001.  
 XX  
 XX PF 10-JAN-2001; 2001WO-US000798.  
 XX  
 XX PR 14-JAN-2000; 2000US-0176077P.  
 XX PR 14-MAR-2000; 2000US-0189167P.  
 XX PR 24-MAR-2000; 2000US-0192099P.  
 XX PR 29-MAR-2000; 2000US-0193480P.  
 XX PR 15-MAY-2000; 2000US-0205230P.  
 XX PR 09-JUN-2000; 2000US-0211315P.  
 XX PR 25-JUL-2000; 2000US-0220534P.  
 XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 XX Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX  
 XX WPI; 2001-451856/48.  
 XX  
 XX New peptide useful as a marker for the diagnosis of breast cancer.  
 XX  
 XX Claim 1; Page 2821; 3695pp; English.  
 XX  
 XX The invention relates to human breast cancer expressed polynucleotides  
 XX (AAL07544-AAL26789) and methods of assessing whether a patient is  
 XX afflicted with breast cancer by examining the correlation between the  
 XX expression of certain markers and the cancerous state of breast cells.  
 XX The polynucleotides and encoded polypeptides are potential markers for  
 XX detecting, diagnosing, monitoring, characterising treating and  
 XX potentially preventing breast cancer. The polynucleotides and encoded  
 XX polypeptides are also useful for isolating compounds with cytostatic  
 XX activity  
 XX  
 XX Sequence 284 BP; 75 A; 65 C; 52 G; 92 T; 0 U; 0 Other;  
 XX  
 XX Query Match 100.0%; Score 11; DB 4; Length 284;  
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 CTTTGGCACTA 11  
 XX |||||  
 XX Db 105 CTTTGGCACTA 115  
 XX  
 XX RESULT 50  
 XX AAS60629/c  
 XX ID AAS60629 standard; cDNA; 286 BP.  
 XX  
 XX AC AAS60629;  
 XX  
 XX 29-JAN-2002 (first entry)  
 XX  
 XX DE Human cancer agent-resistance marker #384.  
 XX  
 XX KW Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;  
 XX squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;  
 XX lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;  
 XX Hodgkin's disease; glioma; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX WO200179556-A2.  
 XX  
 XX PD 25-OCT-2001.  
 XX  
 XX PF 13-APR-2001; 2001WO-US012132.  
 XX  
 XX PR 14-APR-2000; 2000US-0197538P.  
 XX  
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 XX Lillie J, Brown JL, Bolt A, Van Huffel C;  
 XX  
 XX WPI; 2001-602933/68.  
 XX  
 XX Novel nucleic acid, used as a marker to determine the effectiveness of  
 XX using TAXOL to treat cancer cell growth in individuals.  
 XX  
 XX Claim 1; Page 262; 527pp; English.  
 XX  
 XX The invention relates to 1046 novel nucleic acids which are used as  
 XX markers for determining the sensitivity of a cancer cell to the  
 XX anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they  
 XX are shown to express one of the 242 sensitivity markers or the cells are  
 XX shown not to express one of the 804 resistance markers. The methods can  
 XX be used to determine the effectiveness of TAXOL in the treatment of  
 XX

CC cancer cell growth in an individual. The markers can be used as targets  
CC in developing anti-cancer agents such as chemotherapeutic compounds. The  
CC markers can also be used as targets in developing treatments for cancer,  
CC particularly those cancers which display resistance to agents and exhibit  
CC expression of the markers. The anticancer agents developed by the novel  
CC method can be used to treat cancer. Probes based on the markers can be  
CC used to detect transcripts or genomic sequences corresponding to the  
CC markers, in the identification of cells or tissues which mis-express the  
CC protein. Cancers which may be targeted include carcinoma (e.g. squamous  
CC cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic  
CC leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's  
CC disease and tumours (e.g. glioma). The present sequence is one of the  
CC 1046 novel cancer cell markers  
XX

SQ Sequence 286 BP; 95 A; 55 C; 62 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 286;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11  
|||  
Db 192 CTTTGGCACTA 182

Search completed: March 12, 2005, 10:04:52  
Job time : 266 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 10:04:58 ; Search time 56.5 Seconds  
(without alignments)  
150.597 Million cell updates/sec

Title: US-10-070-588a-112

Perfect score: 3

Sequence: 1 ctttggcacta 11

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3949848

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:  
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-O=/cgn2\_1/USFPO\_spool/US10070588/runat\_10032005\_120704\_15234/app\_query.fasta\_1.199  
-DB=A\_Geneseq\_16Dec04 -QWTFastan -SUFFIX=oligo -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human4.0.cdi  
-LIST=500 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USR=US10070588 @CGN 1 1 137 @runat\_10032005\_120704\_15234 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :  
1: Geneseq\_16Dec04:  
A: Geneseq\_1980s:  
2: Geneseq\_1980s:  
3: Geneseq\_2000s:  
4: Geneseq\_2001s:  
5: Geneseq\_2002s:  
6: Geneseq\_2003as:  
7: Geneseq\_2003bs:  
8: Geneseq\_2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	3	100.0	8	1	AA81949 8 amino a
2	3	100.0	8	2	AA35903 Hepatitis
3	3	100.0	8	2	AA35885 Hepatitis
4	3	100.0	8	2	AA35884 Hepatitis
5	3	100.0	8	2	AA35882 Hepatitis
6	3	100.0	8	2	AA35883 Hepatitis
7	3	100.0	8	2	AA42565 Tri-/tetra
8	3	100.0	8	2	AA35898 N-termina
9	3	100.0	8	2	AA73487 Human TSH
10	3	100.0	8	2	AA73488 Human TSH

11	3	100.0	8	2	AA73476 Human TSH
12	3	100.0	8	2	AA73413 Human TSH
13	3	100.0	8	2	AA73414 Human TSH
14	3	100.0	8	2	AA73474 Human TSH
15	3	100.0	8	2	AA73475 Human TSH
16	3	100.0	8	2	AA73489 Human TSH
17	3	100.0	8	2	AA73412 Human TSH
18	3	100.0	8	2	AA84449 Hepatitis
19	3	100.0	8	2	AA84450 Hepatitis
20	3	100.0	8	2	ADC81358 Bovin THF
21	3	100.0	8	2	AAW36922 Peptide e
22	3	100.0	8	2	AAW36925 Peptide e
23	3	100.0	8	2	AAW79266 Bovine gl
24	3	100.0	8	2	AAW56853 Enzyme in
25	3	100.0	8	2	AAW75829 Mouse mas
26	3	100.0	8	2	AAW20315 Human mic
27	3	100.0	8	2	AAW59492 Human pro
28	3	100.0	8	2	AAW78686 SH2 domain
29	3	100.0	8	2	AAW78521 SH2 domain
30	3	100.0	8	2	AAW67227 aPL immun
31	3	100.0	8	2	AAW67141 Antibody
32	3	100.0	8	2	AAW29699 TNF recep
33	3	100.0	8	2	AAW29698 TNF recep
34	3	100.0	8	2	AAW29700 TNF recep
35	3	100.0	8	2	AAW29697 TNF recep
36	3	100.0	8	2	AAW47925 Human MHC
37	3	100.0	8	2	AAW67654 LXXLL eig
38	3	100.0	8	2	AAW16865 Heat shoc
39	3	100.0	8	2	AAW16846 Heat shoc
40	3	100.0	8	2	AAW93856 Mouse BR9
41	3	100.0	8	3	AAW28324 Human sec
42	3	100.0	8	3	AAW69116 Subsequen
43	3	100.0	8	3	AAW69128 Subsequen
44	3	100.0	8	3	AAW84485 Amino aci
45	3	100.0	8	3	AAW84484 Amino aci
46	3	100.0	8	3	AAW84483 Amino aci
47	3	100.0	8	3	AAW84500 Amino aci
48	3	100.0	8	3	AAW84489 Amino aci
49	3	100.0	8	3	AAW69217 Tryptic p
50	3	100.0	8	3	AAW29524 E9K pepti
51	3	100.0	8	3	AAW34118 Human sec
52	3	100.0	8	3	AAW21147 Preferred
53	3	100.0	8	3	AAW21145 Preferred
54	3	100.0	8	3	AAW35995 Sorbitol
55	3	100.0	8	3	AAW35815 T7 phage
56	3	100.0	8	3	AAW28150 Alpha-mel
57	3	100.0	8	3	AAW28146 Alpha-mel
58	3	100.0	8	4	AAW88783 Human int
59	3	100.0	8	4	AAW81474 Synthetic
60	3	100.0	8	4	AAW10659 Human Asp
61	3	100.0	8	4	AAW23420 HIV pepti
62	3	100.0	8	4	AAW68496 Human Bre
63	3	100.0	8	4	AAW02611 Human Asp
64	3	100.0	8	4	AAW20363 Mouse pro
65	3	100.0	8	4	AAW65143 Synthetic
66	3	100.0	8	4	AAW75136 Collagena
67	3	100.0	8	4	AAW88960 HER2/neu
68	3	100.0	8	4	AAW8958 HER2/neu
69	3	100.0	8	4	AAW37498 Flagellin
70	3	100.0	8	4	AAW22004 HIV A03 m
71	3	100.0	8	4	AAW22094 HIV A03 m
72	3	100.0	8	4	AAW12087 HIV A02 s
73	3	100.0	8	4	AAW13233 HIV A02 s
74	3	100.0	8	4	AAW13234 HIV A02 s
75	3	100.0	8	4	AAW20019 HIV A03 m
76	3	100.0	8	4	AAW24350 HIV A24 m
77	3	100.0	8	4	AAW14056 HIV A02 s
78	3	100.0	8	4	AAW16447 HIV A24 s
79	3	100.0	8	4	AAW16448 HIV A24 s
80	3	100.0	8	4	AAW11534 HIV A01 s
81	3	100.0	8	4	AAW19597 HIV B62 s
82	3	100.0	8	4	AAW20060 HIV A03 m
83	3	100.0	8	4	AAW22036 HIV A03 m

84	3	100.0	8	4	ABP24334	Abp24334	HIV A24 m	157	3	100.0	8	7	AD123971	Adi233971	A541 locu
85	3	100.0	8	4	ABP24335	Abp24335	HIV A24 m	158	3	100.0	8	7	AD123970	Adi233970	A541 locu
86	3	100.0	8	4	ABP15177	Abp15177	HIV A24 s	159	3	100.0	8	7	ADJ90992	Adj90992	Foot-and-
87	3	100.0	8	4	ABP22422	Abp22422	HIV A11 m	160	3	100.0	8	7	ADJ90993	Adj90993	Foot-and-
88	3	100.0	8	4	ABP14057	Abp14057	HIV A02 s	C 161	3	100.0	8	8	ADH34507	Adh34507	Alpha-mel
89	3	100.0	8	4	ABP16446	Abp16446	HIV A02 s	C 162	3	100.0	8	8	ADG94474	Adg94474	Human JAM
90	3	100.0	8	4	ABP20156	Abp20156	HIV A03 m	C 163	3	100.0	8	8	ADH44539	Adh44539	Animal pr
91	3	100.0	8	4	ABP23849	Abp23849	HIV A01 m	164	3	100.0	8	8	ADH62069	Adh62069	Cyclic an
92	3	100.0	8	4	ABP14058	Abp14058	HIV A02 s	165	3	100.0	8	8	ADH62086	Adh62086	Cyclic an
93	3	100.0	8	4	ABP14061	Abp14061	HIV A02 s	166	3	100.0	8	8	ADH62100	Adh62100	Cyclic an
94	3	100.0	8	4	ABP15206	Abp15206	HIV A24 s	167	3	100.0	8	8	ADH62067	Adh62067	Cyclic an
95	3	100.0	8	4	ABP15032	Abp15032	HIV A03 s	168	3	100.0	8	8	ADH62075	Adh62075	Cyclic an
96	3	100.0	8	4	ABP18188	Abp18188	HIV B58 s	169	3	100.0	8	8	ADH62065	Adh62065	Cyclic an
97	3	100.0	8	4	ABP14059	Abp14059	HIV A02 s	170	3	100.0	8	8	ADH62068	Adh62068	Cyclic an
98	3	100.0	8	4	ABP15031	Abp15031	HIV A03 s	C 171	3	100.0	8	8	ADH76551	Adh76551	Human neu
99	3	100.0	8	4	ABP14060	Abp14060	HIV A02 s	C 172	3	100.0	8	8	ADJ72154	Adj72154	Cyclin re
100	3	100.0	8	4	ABP12062	Abp12062	HIV A02 s	C 173	3	100.0	8	8	ADJ72147	Adj72147	Cyclin re
101	3	100.0	8	4	ABP12088	Abp12088	HIV A02 s	C 174	3	100.0	8	8	ADJ78900	Adj78900	Peptide #
102	3	100.0	8	4	ABP12086	Abp12086	HIV A02 s	C 175	3	100.0	8	8	ADJ78905	Adj78905	Peptide #
103	3	100.0	8	4	ABP23894	Abp23894	HIV A11 m	C 176	3	100.0	8	8	ADJ78899	Adj78899	Peptide #
104	3	100.0	8	4	ABP17722	Abp17722	HIV B58 s	C 177	3	100.0	8	8	ADJ78907	Adj78907	Peptide #
105	3	100.0	8	4	ABP15205	Abp15205	HIV A24 s	C 178	3	100.0	8	8	ADJ78893	Adj78893	Peptide #
106	3	100.0	8	4	ABP16445	Abp16445	HIV A24 s	C 179	3	100.0	8	8	ADJ78898	Adj78898	Peptide #
107	3	100.0	8	4	ABP18392	Abp18392	HIV B58 s	C 180	3	100.0	8	8	ADJ78895	Adj78895	Peptide #
108	3	100.0	8	4	ABP18591	Abp18591	HIV B62 s	C 181	3	100.0	8	8	ADJ78901	Adj78901	Peptide #
109	3	100.0	8	4	AA80496	Aa80496	PTH2 rece	C 182	3	100.0	8	8	ADJ78902	Adj78902	Peptide #
110	3	100.0	8	4	AAJ00571	Aaj00571	Hepatitis	C 183	3	100.0	8	8	ADJ78894	Adj78894	Peptide #
111	3	100.0	8	4	AAJ01167	Aaj01167	Hepatitis	C 184	3	100.0	8	8	ADJ78896	Adj78896	Peptide #
112	3	100.0	8	4	AAJ01699	Aaj01699	Hepatitis	C 185	3	100.0	8	8	ADJ78892	Adj78892	Peptide #
113	3	100.0	8	4	AAJ00550	Aaj00550	Hepatitis	C 186	3	100.0	8	8	ADJ78897	Adj78897	Peptide #
114	3	100.0	8	4	AAJ00399	Aaj00399	Hepatitis	C 187	3	100.0	8	8	ADJ78903	Adj78903	Peptide #
115	3	100.0	8	4	AAJ00933	Aaj00933	Hepatitis	C 188	3	100.0	8	8	ADJ78904	Adj78904	Peptide #
116	3	100.0	8	4	AAJ01326	Aaj01326	Hepatitis	C 189	3	100.0	8	8	ADJ78906	Adj78906	Peptide #
117	3	100.0	8	4	AAJ01732	Aaj01732	Hepatitis	C 190	3	100.0	8	8	ADI46873	Adi46873	Permeabil
118	3	100.0	8	4	AAJ01023	Aaj01023	Hepatitis	C 191	3	100.0	8	8	ADK08449	Adk08449	Human pap
119	3	100.0	8	4	AAJ00406	Aaj00406	Hepatitis	C 192	3	100.0	8	8	ADK10015	Adk10015	Human pap
120	3	100.0	8	4	AAJ01654	Aaj01654	Hepatitis	C 193	3	100.0	8	8	ADK08872	Adk08872	Human pap
121	3	100.0	8	5	AAE25496	Aae25496	Enzyme cl	C 194	3	100.0	8	8	ADK09291	Adk09291	Human pap
122	3	100.0	8	5	AAE25496	Aae25496	CAP1-29 t	C 195	3	100.0	8	8	ADK08841	Adk08841	Human pap
123	3	100.0	8	5	ABG71053	Abg71053	Tumour ne	C 196	3	100.0	8	8	ADK08873	Adk08873	Human pap
124	3	100.0	8	5	ABG71053	Abg71053	Tumour ne	C 197	3	100.0	8	8	ADK10131	Adk10131	Human pap
125	3	100.0	8	5	ABG71050	Abg71050	Tumour ne	C 198	3	100.0	8	8	ADK08088	Adk08088	Human pap
126	3	100.0	8	5	ABG35001	Abg35001	Human pro	C 199	3	100.0	8	8	ADK10830	Adk10830	Human pap
127	3	100.0	8	5	AAE26705	Aae26705	Matrix me	C 200	3	100.0	8	8	ADK03860	Adk03860	Hepatitis
128	3	100.0	8	5	ABP53319	Abp53319	Alpha-mel	C 201	3	100.0	8	8	ADL95921	Adl95921	Antibody-
129	3	100.0	8	5	ABP78620	Abp78620	Human Asp	C 202	3	100.0	8	8	ADM73301	Adm73301	Human SCP
130	3	100.0	8	5	ABG67499	Abg67499	Human ADP	C 203	3	100.0	8	8	ADM73308	Adm73308	Human SCP
131	3	100.0	8	5	AAE25169	Aae25169	Mouse BR9	C 204	3	100.0	8	8	ADM68731	Adm68731	Human MAG
132	3	100.0	8	5	ABG98330	Abg98330	Secreted	C 205	3	100.0	8	8	ADP67890	Adp67890	Anti-micr
133	3	100.0	8	6	ABJ19705	Abj19705	Human sec	C 206	3	100.0	8	8	ADP67915	Adp67915	Anti-micr
134	3	100.0	8	6	ABJ19705	Abj19705	Factor II	C 207	3	100.0	8	8	ADP67880	Adp67880	Anti-micr
135	3	100.0	8	6	ABP99691	Abp99691	Human sec	C 208	3	100.0	8	8	ADP67883	Adp67883	Anti-micr
136	3	100.0	8	6	ABJ20077	Abj20077	MHC bindi	C 209	3	100.0	8	8	ADP67901	Adp67901	Anti-micr
137	3	100.0	8	6	ABR01171	Abro1171	Human gen	C 210	3	100.0	8	8	ADP67884	Adp67884	Anti-micr
138	3	100.0	8	6	ABP74652	Abp74652	Human SCP	C 211	3	100.0	8	8	ADP67882	Adp67882	Anti-micr
139	3	100.0	8	6	ADA44124	Ada44124	Human sec	C 212	3	100.0	8	8	ADP87049	Adp87049	Junctiona
140	3	100.0	8	6	ADA23613	Ada23613	Alzheimer	C 213	3	100.0	8	8	ADQ28101	Adq28101	Excluded
141	3	100.0	8	6	ABR62780	Abro62780	Alpha-MSH	C 214	3	100.0	8	8	ADQ28102	Adq28102	Excluded
142	3	100.0	8	7	ADC20459	Adc20459	Human sec	C 215	3	100.0	8	8	ADQ28109	Adq28109	Excluded
143	3	100.0	8	7	ADC09511	Adc09511	Epitope w	C 216	3	100.0	8	8	ADQ28103	Adq28103	Excluded
144	3	100.0	8	7	ADC33665	Adc33665	Matrix me	C 217	3	100.0	8	8	ADQ28118	Adq28118	Excluded
145	3	100.0	8	7	AAE39184	Aae39184	Angiogene	C 218	3	100.0	8	8	ADQ28128	Adq28128	Excluded
146	3	100.0	8	7	ADC15558	Adc15558	Rho 110 1	C 219	3	100.0	8	8	ADQ28099	Adq28099	Excluded
147	3	100.0	8	7	ABW00631	Abw00631	Mouse BR6	C 220	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
148	3	100.0	8	7	ADD57117	Add57117	HLA bindi	C 221	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
149	3	100.0	8	7	ADD57541	Add57541	HLA bindi	C 222	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
150	3	100.0	8	7	ADD58002	Add58002	HLA bindi	C 223	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
151	3	100.0	8	7	ADD23843	Add23843	Breast ca	C 224	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
152	3	100.0	8	7	ADD15711	Add15711	Peptide 1	C 225	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
153	3	100.0	8	7	ADD15704	Add15704	Peptide 1	C 226	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
154	3	100.0	8	7	ABW02758	Abw02758	Angiogene	C 227	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
155	3	100.0	8	7	ADG72970	Adg72970	Heat choc	C 228	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
156	3	100.0	8	7	ADG72951	Adg72951	Heat choc	C 229	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an

230	3	100.0	9	2	AAR59218	Peptide f	303	3	100.0	9	2	AAW62730	Streptoco
231	3	100.0	9	2	AAR59199	Peptide f	C 304	3	100.0	9	2	AAW77279	P. damsel
232	3	100.0	9	2	AAR59172	Peptide f	C 305	3	100.0	9	2	AAW20755	Human neu
233	3	100.0	9	2	AAR61691	HLA-A2, 1	C 306	3	100.0	9	2	AAW21455	Human neu
234	3	100.0	9	2	AAR58764	Peptide i	C 307	3	100.0	9	2	AAW54608	Peptide 1
235	3	100.0	9	2	AAR56351	Peptide i	C 308	3	100.0	9	2	AAW54646	Peptide f
236	3	100.0	9	2	AAR56364	Peptide i	C 309	3	100.0	9	2	AAW78836	BAGE prot
237	3	100.0	9	2	AAR56340	Peptide i	C 310	3	100.0	9	2	AAW60009	HA-2 mino
238	3	100.0	9	2	AAR56376	Peptide i	C 311	3	100.0	9	2	AAW77129	BAGE svnt
239	3	100.0	9	2	AAR56373	Peptide i	C 312	3	100.0	9	2	AAW68375	Human BAG
240	3	100.0	9	2	AAR56377	Peptide i	C 313	3	100.0	9	2	AAW46066	Antiphosp
241	3	100.0	9	2	AAR56366	Peptide i	C 314	3	100.0	9	2	AAW67101	Antibody
242	3	100.0	9	2	AAR56379	Peptide i	C 315	3	100.0	9	2	AAW67118	Antibody
243	3	100.0	9	2	AAR56318	Peptide i	C 316	3	100.0	9	2	AAW46351	Amino aci
244	3	100.0	9	2	AAR56326	Peptide i	C 317	3	100.0	9	2	AAW46349	Amino aci
245	3	100.0	9	2	AAR56346	Peptide i	C 318	3	100.0	9	2	AAW46350	Amino aci
246	3	100.0	9	2	AAR56358	Peptide i	C 319	3	100.0	9	2	AAW47937	AE101 ana
247	3	100.0	9	2	AAR56360	Peptide i	C 320	3	100.0	9	2	AAW97954	Human syn
248	3	100.0	9	2	AAR56330	Peptide i	C 321	3	100.0	9	2	AAW10524	HLA Class
249	3	100.0	9	2	AAR56372	Peptide i	C 322	3	100.0	9	2	AAW10636	Peptide a
250	3	100.0	9	2	AAR56370	Peptide i	C 323	3	100.0	9	2	AAW40233	Amino aci
251	3	100.0	9	2	AAR56363	Peptide i	C 324	3	100.0	9	2	AAW47487	Immunogen
252	3	100.0	9	2	AAR56367	Peptide i	C 325	3	100.0	9	2	AAW47812	Immunogen
253	3	100.0	9	2	AAR56371	Peptide i	C 326	3	100.0	9	2	AAW46853	Immunogen
254	3	100.0	9	2	AAR56375	Peptide i	C 327	3	100.0	9	2	AAW46855	Immunogen
255	3	100.0	9	2	AAR56317	Peptide i	C 328	3	100.0	9	2	AAW46021	Immunogen
256	3	100.0	9	2	AAR56320	Peptide i	C 329	3	100.0	9	2	AAW47488	Immunogen
257	3	100.0	9	2	AAR56327	Peptide i	C 330	3	100.0	9	2	AAW47767	Immunogen
258	3	100.0	9	2	AAR56329	Peptide i	C 331	3	100.0	9	2	AAW46424	Immunogen
259	3	100.0	9	2	AAR56341	Peptide i	C 332	3	100.0	9	2	AAW46891	Immunogen
260	3	100.0	9	2	AAR56349	Peptide i	C 333	3	100.0	9	2	AAW47722	Immunogen
261	3	100.0	9	2	AAR56359	Peptide i	C 334	3	100.0	9	2	AAW46487	Immunogen
262	3	100.0	9	2	AAR56361	Peptide i	C 335	3	100.0	9	2	AAW47727	Immunogen
263	3	100.0	9	2	AAR56368	Peptide i	C 336	3	100.0	9	2	AAW46776	Immunogen
264	3	100.0	9	2	AAR56325	Peptide i	C 337	3	100.0	9	2	AAW46675	Immunogen
265	3	100.0	9	2	AAR56339	Peptide i	C 338	3	100.0	9	2	AAW03665	Amino aci
266	3	100.0	9	2	AAR56345	Peptide i	C 339	3	100.0	9	2	AAW93921	Synthetic
267	3	100.0	9	2	AAR56322	Peptide i	C 340	3	100.0	9	2	AAW93918	Synthetic
268	3	100.0	9	2	AAR56343	Peptide i	C 341	3	100.0	9	2	AAW93938	Synthetic
269	3	100.0	9	2	AAR56347	Peptide i	C 342	3	100.0	9	2	AAW67675	Mutated L
270	3	100.0	9	2	AAR56348	Peptide i	C 343	3	100.0	9	2	AAW33152	Human BAG
271	3	100.0	9	2	AAR56369	Peptide i	C 344	3	100.0	9	2	AAW25276	HIV Env g
272	3	100.0	9	2	AAR56332	Peptide i	C 345	3	100.0	9	2	AAW25241	HIV pol p
273	3	100.0	9	2	AAR56378	Peptide i	C 346	3	100.0	9	2	AAW25275	HIV Env g
274	3	100.0	9	2	AAR56342	Peptide i	C 347	3	100.0	9	2	AAW25242	HIV pol p
275	3	100.0	9	2	AAR56319	Peptide i	C 348	3	100.0	9	2	AAW89112	ScFV (dig
276	3	100.0	9	2	AAR56324	Peptide i	C 349	3	100.0	9	2	AAW53546	Human BAG
277	3	100.0	9	2	AAR56344	Peptide i	C 350	3	100.0	9	2	AAW00811	HLA-A24 a
278	3	100.0	9	2	AAR56350	Peptide i	C 351	3	100.0	9	2	AAW26889	Tumour-de
279	3	100.0	9	2	AAR56323	Peptide i	C 352	3	100.0	9	2	AAW97259	Cytotoxic
280	3	100.0	9	2	AAR56374	Peptide i	C 353	3	100.0	9	2	AAW00690	Tumour an
281	3	100.0	9	2	AAR56331	Peptide i	C 354	3	100.0	9	2	AAW31777	Mycobacte
282	3	100.0	9	2	AAR56380	Peptide i	C 355	3	100.0	9	2	AAW31775	Mycobacte
283	3	100.0	9	2	AAR69862	Peptide f	C 356	3	100.0	9	2	AAW49642	Tumour an
284	3	100.0	9	2	AAR87312	Plasmodi	C 357	3	100.0	9	2	AAW05025	Tumour an
285	3	100.0	9	2	AAR87269	Antialler	C 358	3	100.0	9	2	AAW96727	IL-8 deri
286	3	100.0	9	2	AAR69800	Human MHC	C 359	3	100.0	9	2	AAW01732	Exemplary
287	3	100.0	9	2	AAR87432	HLA-C-clo	C 360	3	100.0	9	2	AAW43100	Chondroge
288	3	100.0	9	2	AAR89909	HLA-C-clo	C 361	3	100.0	9	2	AAW94132	Peptide i
289	3	100.0	9	2	AAR67810	BAGE tumo	C 362	3	100.0	9	3	AAW71499	Human BAG
290	3	100.0	9	2	AAR84331	HPV deriv	C 363	3	100.0	9	3	AAW94359	Human 5T4
291	3	100.0	9	2	AAR72807	FOK1 tryp	C 364	3	100.0	9	3	AAW94373	Mouse 5T4
292	3	100.0	9	2	AAR80577	CTR1 berl	C 365	3	100.0	9	3	AAW78999	Urokinase
293	3	100.0	9	2	AAR66491	FOK1 rest	C 366	3	100.0	9	3	AAW90783	Human leu
294	3	100.0	9	2	AAW02153	BAGE tumo	C 367	3	100.0	9	3	AAW70832	BH3 domai
295	3	100.0	9	2	AAW02154	BAGE tumo	C 368	3	100.0	9	3	AAW13745	Peptide f
296	3	100.0	9	2	AAW28811	HPV-16 de	C 369	3	100.0	9	3	AAW18492	Peptide s
297	3	100.0	9	2	AAW14505	HLA-A2, 1-	C 370	3	100.0	9	3	AAW98634	wt1 deriv
298	3	100.0	9	2	AAW36923	Peptide e	C 371	3	100.0	9	3	AAW33648	MHC class
299	3	100.0	9	2	AAW36926	Peptide e	C 372	3	100.0	9	3	AAW23664	Cytotoxic
300	3	100.0	9	2	AAW22040	Antigenic	C 373	3	100.0	9	3	AAW20817	D box pep
301	3	100.0	9	2	AAW10399	Antiphosp	C 374	3	100.0	9	3	AAW92279	BAGE ant1
302	3	100.0	9	2	AAW10275	Antiphosp	C 375	3	100.0	9	3	AAW66446	HLA-A2-bi

376	3	100.0	9	3	AAV56595	BAGE gene	449	3	100.0	9	4	AAU24428	Human MHC
377	3	100.0	9	3	AAV76692	SCP-1 HLA	450	3	100.0	9	4	AAU24338	Human MHC
378	3	100.0	9	3	AAV09899	Human gly	C 451	3	100.0	9	4	AAU19891	Neisseria
379	3	100.0	9	3	AAU14892	MCA subet	452	3	100.0	9	4	AAU75866	Influenza
380	3	100.0	9	3	AAU95994	Human MHC	C 453	3	100.0	9	4	AAU03310	Fruit fly
381	3	100.0	9	3	AAU84275	Tumour as	454	3	100.0	9	4	AAU31324	Exemplary
382	3	100.0	9	3	AAU82958	BAGE tumo	C 455	3	100.0	9	4	AAU37497	Flagellin
383	3	100.0	9	3	AAU02601	Tumour as	456	3	100.0	9	4	ABP16468	HIV A24 s
384	3	100.0	9	3	AAV67271	MMP3 subs	457	3	100.0	9	4	ABP22010	HIV A03 m
385	3	100.0	9	3	AAU08673	Antigenic	458	3	100.0	9	4	ABP12233	HIV A02 s
386	3	100.0	9	3	AAU26353	Human CAS	459	3	100.0	9	4	ABP14095	HIV A02 s
387	3	100.0	9	3	AAU26346	Human CAS	460	3	100.0	9	4	ABP12234	HIV A02 s
388	3	100.0	9	3	AAU26358	Human CAS	461	3	100.0	9	4	ABP15043	HIV A03 s
389	3	100.0	9	3	AAU26364	Human CAS	462	3	100.0	9	4	ABP20065	HIV A03 m
390	3	100.0	9	3	AAU26330	Human CAS	463	3	100.0	9	4	ABP12212	HIV A02 s
391	3	100.0	9	3	AAU32276	HLA A0201	464	3	100.0	9	4	ABP11570	HIV A01 s
392	3	100.0	9	3	AAU32264	HLA A0201	465	3	100.0	9	4	ABP15314	HIV A24 s
393	3	100.0	9	3	AAU08324	Epitope d	466	3	100.0	9	4	ABP12210	HIV A02 s
394	3	100.0	9	3	AAU68958	Human TAD	467	3	100.0	9	4	ABP14094	HIV A02 s
395	3	100.0	9	3	AAU68946	Human TAD	468	3	100.0	9	4	ABP15044	HIV A03 s
396	3	100.0	9	3	AAU88782	Human int	469	3	100.0	9	4	ABP22497	HIV A11 m
397	3	100.0	9	3	AAU23477	HIV pepti	470	3	100.0	9	4	ABP14090	HIV A02 s
398	3	100.0	9	3	AAU23447	HIV pepti	471	3	100.0	9	4	ABP20045	HIV A03 m
399	3	100.0	9	3	AAU22224	HIV pepti	472	3	100.0	9	4	ABP21987	HIV A02 s
400	3	100.0	9	3	AAU23460	HIV pepti	473	3	100.0	9	4	ABP14092	HIV A02 s
401	3	100.0	9	3	AAU23445	HIV pepti	474	3	100.0	9	4	ABP15313	HIV A24 s
402	3	100.0	9	3	AAU23427	HIV pepti	475	3	100.0	9	4	ABP22096	HIV A03 m
403	3	100.0	9	3	AAU23428	HIV pepti	476	3	100.0	9	4	ABP23896	HIV A11 m
404	3	100.0	9	3	AAU23459	HIV pepti	477	3	100.0	9	4	ABP14093	HIV A02 s
405	3	100.0	9	3	AAU23479	HIV pepti	478	3	100.0	9	4	ABP15312	HIV A24 s
406	3	100.0	9	3	AAU95946	Vaccine r	479	3	100.0	9	4	ABP16030	HIV A24 s
407	3	100.0	9	3	AAU00185	Laccase r	480	3	100.0	9	4	ABP20112	HIV A03 m
408	3	100.0	9	3	AAU00170	Laccase a	481	3	100.0	9	4	ABP22009	HIV A03 m
409	3	100.0	9	3	AAU00066	Savinas a	482	3	100.0	9	4	ABP22042	HIV A03 m
410	3	100.0	9	3	AAU00054	Savinas a	483	3	100.0	9	4	ABP23854	HIV A11 m
411	3	100.0	9	3	AAU46082	Human TF	484	3	100.0	9	4	ABP13232	HIV A02 s
412	3	100.0	9	3	AAU75673	HLA class	485	3	100.0	9	4	ABP12231	HIV A02 s
413	3	100.0	9	3	AAU75634	HLA class	486	3	100.0	9	4	ABP12232	HIV A02 s
414	3	100.0	9	3	AAU75634	HLA class	487	3	100.0	9	4	ABP17683	HIV B58 s
415	3	100.0	9	3	AAU70064	BAGE huma	488	3	100.0	9	4	ABP14091	HIV A03 s
416	3	100.0	9	3	AAU70073	Human cal	489	3	100.0	9	4	ABP17625	HIV B58 s
417	3	100.0	9	3	AAU70036	Human cal	490	3	100.0	9	4	ABP22144	HIV A03 m
418	3	100.0	9	3	AAU70045	Human cal	491	3	100.0	9	4	ABP22144	HIV A03 m
419	3	100.0	9	3	AAU70060	Human cal	492	3	100.0	9	4	ABP13432	HIV A02 s
420	3	100.0	9	3	AAU70018	Human cal	493	3	100.0	9	4	ABP24348	HIV A24 m
421	3	100.0	9	3	AAU70011	Human cal	494	3	100.0	9	4	AAU68733	Human Wil
422	3	100.0	9	3	AAU70015	Human cal	C 495	3	100.0	9	4	AAU45872	Human tum
423	3	100.0	9	3	AAU68699	Major out	496	3	100.0	9	4	AAU02236	HLA bindi
424	3	100.0	9	3	AAU95894	MHC class	497	3	100.0	9	4	AAU02274	HLA bindi
425	3	100.0	9	3	AAU93744	Human PUM	498	3	100.0	9	4	AAU02239	HLA bindi
426	3	100.0	9	3	AAU47343	Epithelia	499	3	100.0	9	4	AAU02263	HLA bindi
427	3	100.0	9	3	AAU88385	HER2/NEU	500	3	100.0	9	4	AAU02293	HLA bindi
428	3	100.0	9	3	AAU88479	HER2/NEU							
429	3	100.0	9	3	AAU88657	HER2/NEU							
430	3	100.0	9	3	AAU88445	HER2/NEU							
431	3	100.0	9	3	AAU88959	HER2/NEU							
432	3	100.0	9	3	AAU88457	HER2/NEU							
433	3	100.0	9	3	AAU88591	HER2/NEU							
434	3	100.0	9	3	AAU88525	HER2/NEU							
435	3	100.0	9	3	AAU60146	Matrix me							
436	3	100.0	9	3	AAU68668	HER-2 CTL							
437	3	100.0	9	3	AAU07553	Human PUM							
438	3	100.0	9	3	AAU07642	Human PUM							
439	3	100.0	9	3	AAU99417	PRAME der							
440	3	100.0	9	3	AAU99435	PRAME der							
441	3	100.0	9	3	AAU01556	Human SSX							
442	3	100.0	9	3	AAU46273	HPV type							
443	3	100.0	9	3	AAU61966	Human WT1							
444	3	100.0	9	3	AAU08243	Human str							
445	3	100.0	9	3	AAU08251	Human str							
446	3	100.0	9	3	AAU08248	Human str							
447	3	100.0	9	3	AAU23840	Human MHC							
448	3	100.0	9	3	AAU24232	Human MHC							

## ALIGNMENTS

## RESULT 1

AAU1949  
ID AAP81949 standard; protein; 8 AA.  
XX  
AC AAP81949;  
XX

XX  
DT 25-MAR-2003 (revised)  
DT 15-OCT-1990 (first entry)  
XX

XX  
DE 8 amino acid peptide fragment of pure sorbine.  
DE

XX  
KW sorbine; water and sodium absorption; diarrhoea; pig intestinal mucosa.  
KW

XX  
OS Sus scrofa.  
OS

XX  
FN FR2601020-A.  
FN



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PD 08-JAN-1988.
PF 03-JUL-1986; 86FR-00609682.
XX
XX 03-JUL-1986; 86FR-00009682.
XX (INRM ) INSERM INST NAT SANTE & RECH MED.
XX Vagnedeser M, Panuescla D, Mutt V, Jornvall H;
XX WPI; 1988-058509/09.
XX
XX New polypeptide sorbose stimulating water and sodium absorption - by the
PT intestine, and its fragments, useful for treating diarrhoea.
XX
XX Claim 3; Page 19; 21pp; French.
XX
XX Fragment forms part of sorbine as purified from pig intestinal mucosa.
CC The final order of the fragments in the intact polypeptide is not known.
CC It is thought, however, that this fragment is the fifth (starting at the
CC N-terminal) in the sequence. see also AAP81945-8 and AAP81950-P81952.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x AAP81949 (1-8)

Qy 10 AGTGCCAAA 2
Db 1 SerAlalys 3

RESULT 2
AAR35903
ID AAR35903 standard; protein; 8 AA.
XX
AC AAR35903;
XX
XX 25-MAR-2003 (revised)
DT 24-MAY-1993 (first entry)
XX
XX Hepatitis C virus (HCV) epitope.
XX
XX Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW infection.
XX
OS Hepatitis C virus type 1.
XX
XX WO9300365-A2.
XX
XX 07-JAN-1993.
XX
XX 24-JUN-1992; 92WO-US005388.
XX
XX 24-JUN-1991; 91US-00722489.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chien DY, Rutter W;
XX
XX WPI; 1993-036334/04.
XX
XX Polypeptide(s) comprising truncated hepatitis C virus sequences - for
PT detection, prevention and treatment of hepatitis C infection.
XX
XX Example A; Page 35; 80pp; English.
XX
XX This octamer was found to be immunoreactive with anti-HCV anti-sera. In
CC the epitope mapping experiment three different samples of anti-sera were
CC reacted with the peptide octamer, and then incubated with HRP-labelled
CC goat anti-human Ig antiser, to enable detection of binding. This epitope
CC starts from amino acid 613 of the HCV polypeptide. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR35903 (1-8)

Qy 3 TTGCGACTA 11
Db 1 LeuAlaLeu 3

RESULT 3
AAR35885
ID AAR35885 standard; protein; 8 AA.
XX
AC AAR35885;
XX
XX 25-MAR-2003 (revised)
DT 24-MAY-1993 (first entry)
XX
XX Hepatitis C virus (HCV) epitope.
XX
XX Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW infection.
XX
OS Hepatitis C virus type 1.
XX
XX WO9300365-A2.
XX
XX 07-JAN-1993.
XX
XX 24-JUN-1992; 92WO-US005388.
XX
XX 24-JUN-1991; 91US-00722489.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chien DY, Rutter W;
XX
XX WPI; 1993-036334/04.
XX
XX Polypeptide(s) comprising truncated hepatitis C virus sequences - for
PT detection, prevention and treatment of hepatitis C infection.
XX
XX Example A; Page 35; 80pp; English.
XX
XX This octamer was found to be immunoreactive with anti-HCV anti-sera. In
CC the epitope mapping experiment three different samples of anti-sera were
CC reacted with the peptide octamer, and then incubated with HRP-labelled
CC goat anti-human Ig antiser, to enable detection of binding. This epitope
CC starts from amino acid 613 of the HCV polypeptide. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 8 AA;

Alignment Scores:

```

Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR35885 (1-8)

QY 1 CTTTGGCAC 9  
 |||||  
 Db 3 LeuTrpHis 5

# RESULT 4

AAR35884  
 ID AAR35884 standard; protein; 8 AA.

XX AC AAR35884;

XX DT 25-MAR-2003 (revised)  
 XX DT 24-MAY-1993 (first entry)

XX DE Hepatitis C virus (HCV) epitope.

XX KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;  
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;  
 XX infection.

XX OS Hepatitis C virus type 1.

XX PN WO9300365-A2.

XX PD 07-JAN-1993.

XX PF 24-JUN-1992; 92WO-US005388.

XX PR 24-JUN-1991; 91US-00722489.

XX PA (CHIR ) CHIRON CORP.

XX PI Chien DY, Rutter W;

XX DR WPI; 1993-036334/04.

XX PT Polypeptide(s) comprising truncated hepatitis C virus sequences - for  
 XX detection, prevention and treatment of hepatitis C infection.

XX PS Example A; Page 35; 80pp; English.

XX CC This octamer was found to be immunoreactive with anti-HCV anti-sera. In  
 CC the epitope mapping experiment three different samples of anti-sera were  
 CC reacted with the peptide octamer, and then incubated with HRP-labelled  
 CC goat anti-human Ig anti-sera, to enable detection of binding. This epitope  
 CC starts from amino acid 612 of the HCV polypeptide. (Updated on 25-MAR-  
 XX 2003 to correct PN field.)

XX SQ Sequence 8 AA;

# Alignment Scores:

Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR35884 (1-8)

QY 1 CTTTGGCAC 9  
 |||||  
 Db 4 LeuTrpHis 6

# RESULT 5

AAR35882  
 ID AAR35882 standard; protein; 8 AA.

XX AC AAR35882;

XX DT 25-MAR-2003 (revised)  
 XX DT 24-MAY-1993 (first entry)

XX DE Hepatitis C virus (HCV) epitope.

XX KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;  
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;  
 XX infection.

XX OS Hepatitis C virus type 1.

XX PN WO9300365-A2.

XX PD 07-JAN-1993.

XX PF 24-JUN-1992; 92WO-US005388.

XX PR 24-JUN-1991; 91US-00722489.

XX PA (CHIR ) CHIRON CORP.

XX PI Chien DY, Rutter W;

XX DR WPI; 1993-036334/04.

XX PT Polypeptide(s) comprising truncated hepatitis C virus sequences - for  
 XX detection, prevention and treatment of hepatitis C infection.

XX PS Example A; Page 35; 80pp; English.

XX CC This octamer was found to be immunoreactive with anti-HCV anti-sera. In  
 CC the epitope mapping experiment three different samples of anti-sera were  
 CC reacted with the peptide octamer, and then incubated with HRP-labelled  
 CC goat anti-human Ig anti-sera, to enable detection of binding. This epitope  
 CC starts from amino acid 610 of the HCV polypeptide. (Updated on 25-MAR-  
 XX 2003 to correct PN field.)

XX SQ Sequence 8 AA;

# Alignment Scores:

Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR35882 (1-8)

QY 1 CTTTGGCAC 9  
 |||||  
 Db 6 LeuTrpHis 8

# RESULT 6

AAR35883  
 ID AAR35883 standard; protein; 8 AA.

XX AC AAR35883;

XX DT 25-MAR-2003 (revised)  
 XX DT 24-MAY-1993 (first entry)

XX DE Hepatitis C virus (HCV) epitope FB.

XX KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;  
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;  
 XX infection.

```

OS Hepatitis C virus type 1.
XX WO9300365-A2.
XX
XX 07-JAN-1993.
XX
XX 24-JUN-1992; 92WO-US005388.
XX
XX 24-JUN-1991; 91US-00722489.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chien DY, Rutter W;
XX
XX WPI; 1993-036334/04.
XX
XX Polypeptide(s) comprising truncated hepatitis C virus sequences - for
XX detection, prevention and treatment of hepatitis C infection.
XX
XX Example A; Page 35; 80pp; English.
XX
XX This octamer was found to be immunoreactive with anti-HCV anti-sera. In
XX the epitope mapping experiment three different samples of anti-sera were
XX reacted with the peptide octamer, and then incubated with HRP-labelled
XX goat anti-human Ig antiserum, to enable detection of binding. This epitope
XX starts from amino acid 611 of the HCV polyprotein. This was found to be a
XX particularly strong epitope. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR35883 (1-8)
QY 1 CTTTGGCAC 9
DB 5 LeuTrpHis 7
RESULT 7
AAR42565
ID AAR42565 standard; peptide; 8 AA.
XX
XX AAR42565;
AC
XX
XX 04-NOV-1994 (first entry)
DT
XX
XX Tri-/tetra-cyclic compound linked peptide #9.
DE
XX
XX Tricyclic; tetracyclic; medicament; manufacture; determination;
XX blood platelet thrombi; fibrinogen antagonists.
XX
XX Synthetic.
XX
XX AU9344935-A.
XX
XX 10-MAR-1994.
XX
XX 26-AUG-1993; 93AU-00044935.
XX
XX 31-AUG-1992; 92CH-00002725.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Banwarth W, Gerber F, Griender A, Knierzinger A, Muller K;
XX Obrecht D, Trzeclak A;
XX
XX WPI; 1994-118783/15.
XX
XX New tri- and tetra-cyclic cpds., partic. with peptide chains - used e.g.
XX for determin. of biologically active peptide sequences or as fibrinogen
XX antagonists.
XX
XX Claim 9; Page 120; 131pp; English.
XX
XX The sequences given in AAR42557-68 are peptides which may be linked to
XX the tri- and tetra-cyclic compounds of the invention. These compounds may
XX be used as medicaments or for the manufacture of medicaments. They may
XX esp. be used for the determination of biologically active peptide
XX sequences. Compounds containing the sequence RGDF or RGVV can esp. be
XX used for preventing the formation of blood platelet thrombi, as
XX fibrinogen antagonists
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR42565 (1-8)
QY 3 TTGGCACTA 11
DB 5 LeuAlaLeu 7
RESULT 8
AAR56998
ID AAR56998 standard; peptide; 8 AA.
XX
XX AAR56998;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 15-FEB-1995 (first entry)
DT
XX
XX N-terminal fragment of human histo-blood group A transferase.
DE
XX
XX Blood; group; determinant; antigen; erythrocyte; oligosaccharide;
XX glycoconjugate; glycosphingolipid; glycoprotein; glycosyltransferase;
XX transferase.
XX
XX Homo sapiens.
XX
XX US5326857-A.
XX
XX 05-JUL-1994.
XX
XX 29-AUG-1991; 91US-00752101.
XX
XX 31-AUG-1989; 89US-00402695.
XX
XX (BIOM-) BIOMEMBRANE INST.
XX
XX Hakomori S, Clausen H, Yamamoto F, White T;
XX
XX WPI; 1994-217098/26.
XX
XX Isolated DNA molecules - encode human histo-blood groups A-, B- and O-
XX glycotransferases.
XX
XX Example 2; Col 35; 63pp; English.
XX
XX The histo-blood group ABH determinants are major allogeneic antigens in
XX both erythrocytes and tissues of humans. They generally constitute
XX peripheral parts of the oligosaccharide chains of glycoconjugates
XX i.e. linked to lipids (glycosphingolipids) or to proteins (glycoproteins).
XX It was proposed that the A and B phenotypes were associated with
XX glycosyltransferases that converted the H substance associated with the O

```

CC phenotype to A and B respectively, through the addition of alpha1-3-N-acetylglactosamine or alpha1-3-galactosyl residues to the H antigen Fuc-alpha1-2Gal-beta1-R. Hence, the primary products of the histo-blood group A and B genes are the respective glycosyltransferases. This is a fragment of the A group transferase. See also AAR56995-R57010. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 8 AA;

Alignment Scores:  
Pred. No.: 9.59e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR56998 (1-8)

Qy 9 GTGCCAAAG 1  
|||||||  
Db 6 ValProlys 8

RESULT 9  
AAR73487

ID AAR73487 standard; peptide; 8 AA.

AC AAR73487;

DT 18-DEC-1995 (first entry)

DE Human TSH receptor (residues 573-580).

KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;  
KW affinity; detection.

OS Synthetic.

XX JP07089991-A.

PD 04-APR-1995.

PF 28-SEP-1993; 93JP-00240853.

PR 28-SEP-1993; 93JP-00240853.

PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.

XX WPI; 1995-167251/22.

XX Novel polypeptide(s) having affinity for the human TSH receptor antibody  
PT - used in detection of the TSH antibody.

PS Example 1; Page 41; 54pp; Japanese.

XX Peptides with affinity to human TSH (thyroid stimulating hormone)  
CC receptor antibody are used for detection of the antibody. (See also  
CC AAR73201-592)

XX Sequence 8 AA;

Alignment Scores:  
Pred. No.: 9.59e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR73487 (1-8)

Qy 3 TTGGCACTA 11  
|||||||

Db 6 LeuAlaLeu 8

RESULT 10

AAR73488  
ID AAR73488 standard; peptide; 8 AA.

XX AC AAR73488;

XX 18-DEC-1995 (first entry)

DE Human TSH receptor (residues 575-582).

KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;  
KW affinity; detection.

OS Synthetic.

XX JP07089991-A.

PD 04-APR-1995.

PF 28-SEP-1993; 93JP-00240853.

PR 28-SEP-1993; 93JP-00240853.

PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.

XX WPI; 1995-167251/22.

XX Novel polypeptide(s) having affinity for the human TSH receptor antibody  
PT - used in detection of the TSH antibody.

PS Example 1; Page 41; 54pp; Japanese.

CC Peptides with affinity to human TSH (thyroid stimulating hormone)  
CC receptor antibody are used for detection of the antibody. (See also  
CC AAR73201-592)

XX Sequence 8 AA;

Alignment Scores:  
Pred. No.: 9.59e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR73488 (1-8)

Qy 3 TTGGCACTA 11  
|||||||

Db 4 LeuAlaLeu 6

RESULT 11

AAR73476  
ID AAR73476 standard; peptide; 8 AA.

XX AC AAR73476;

XX 18-DEC-1995 (first entry)

DE Human TSH receptor (residues 551-558).

KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;  
KW affinity; detection.

OS Synthetic.

XX JP07089991-A.

XX 04-APR-1995.

```
PF 28-SEP-1993; 93JP-00240853.
XX
PR 28-SEP-1993; 93JP-00240853.
XX
PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
XX
DR WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX
XX Example 1; Page 39; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73476 (1-8)
Qy 3 TTGGCACTA 11
Db 2 LeuAlaLeu 4
RESULT 12
AAR73413
ID AAR73413 standard; peptide; 8 AA.
XX
AC AAR73413;
XX
XX 12-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 425-432).
XX
XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
XX affinity; detection.
XX
XX Synthetic.
XX
XX JP07089991-A.
XX
XX 04-APR-1995.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX
XX Example 1; Page 32; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73413 (1-8)
Qy 3 TTGGCACTA 11
Db 3 LeuAlaLeu 5
RESULT 13
AAR73414
ID AAR73414 standard; peptide; 8 AA.
XX
AC AAR73414;
XX
XX 12-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 427-434).
XX
XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
XX affinity; detection.
XX
XX Synthetic.
XX
XX JP07089991-A.
XX
XX 04-APR-1995.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX
XX Example 1; Page 32; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73414 (1-8)
Qy 3 TTGGCACTA 11
Db 1 LeuAlaLeu 3
RESULT 14
AAR73474
ID AAR73474 standard; peptide; 8 AA.
XX
AC AAR73474;
XX
XX 18-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 547-554).
DE
```

XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;  
KW affinity; detection.  
XX Synthetic.  
XX JP07089991-A.  
XX  
XX PD 04-APR-1995.  
XX  
XX PF 28-SEP-1993; 93JP-00240853.  
XX  
XX PR 28-SEP-1993; 93JP-00240853.  
XX  
XX PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.  
XX  
XX DR WPI; 1995-167251/22.  
XX  
XX PT Novel polypeptide(s) having affinity for the human TSH receptor antibody  
XX - used in detection of the TSH antibody.  
XX  
XX PS Example 1; Page 39; 54pp; Japanese.  
XX  
XX CC Peptides with affinity to human TSH (thyroid stimulating hormone)  
XX CC receptor antibody are used for detection of the antibody. (See also  
XX CC AAR73201-592)  
XX  
XX SQ Sequence 8 AA;  
XX  
XX Alignment Scores:  
XX Pred. No.: 9.59e+07 Length: 8  
XX Score: 3.00 Matches: 3  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 2 Gaps: 0  
XX  
XX US-10-070-588A-112 (1-11) x AAR73474 (1-8)  
XX  
XX QY 3 TTGGCACTA 11  
XX  
XX DB 6 LeuAlaLeu 8  
XX  
XX RESULT 15  
XX AAR73475  
XX ID AAR73475 standard; peptide; 8 AA.  
XX  
XX AC AAR73475;  
XX  
XX DT 18-DEC-1995 (first entry)  
XX  
XX DE Human TSH receptor (residues 549-556).  
XX  
XX KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;  
XX KW affinity; detection.  
XX  
XX OS Synthetic.  
XX  
XX PN JP07089991-A.  
XX  
XX PD 04-APR-1995.  
XX  
XX PF 28-SEP-1993; 93JP-00240853.  
XX  
XX PR 28-SEP-1993; 93JP-00240853.  
XX  
XX PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.  
XX  
XX DR WPI; 1995-167251/22.  
XX  
XX PT Novel polypeptide(s) having affinity for the human TSH receptor antibody  
XX - used in detection of the TSH antibody.  
XX

PS Example 1; Page 39; 54pp; Japanese.  
XX  
XX CC Peptides with affinity to human TSH (thyroid stimulating hormone)  
XX CC receptor antibody are used for detection of the antibody. (See also  
XX CC AAR73201-592)  
XX  
XX SQ Sequence 8 AA;  
XX  
XX Alignment Scores:  
XX Pred. No.: 9.59e+07 Length: 8  
XX Score: 3.00 Matches: 3  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 2 Gaps: 0  
XX  
XX US-10-070-588A-112 (1-11) x AAR73475 (1-8)  
XX  
XX QY 3 TTGGCACTA 11  
XX  
XX DB 4 LeuAlaLeu 6  
XX  
XX RESULT 16  
XX AAR73489  
XX ID AAR73489 standard; peptide; 8 AA.  
XX  
XX AC AAR73489;  
XX  
XX DT 18-DEC-1995 (first entry)  
XX  
XX DE Human TSH receptor (residues 577-584).  
XX  
XX KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;  
XX KW affinity; detection.  
XX  
XX OS Synthetic.  
XX  
XX PN JP07089991-A.  
XX  
XX PD 04-APR-1995.  
XX  
XX PF 28-SEP-1993; 93JP-00240853.  
XX  
XX PR 28-SEP-1993; 93JP-00240853.  
XX  
XX PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.  
XX  
XX DR WPI; 1995-167251/22.  
XX  
XX PT Novel polypeptide(s) having affinity for the human TSH receptor antibody  
XX - used in detection of the TSH antibody.  
XX  
XX PS Example 1; Page 41; 54pp; Japanese.  
XX  
XX CC Peptides with affinity to human TSH (thyroid stimulating hormone)  
XX CC receptor antibody are used for detection of the antibody. (See also  
XX CC AAR73201-592)  
XX  
XX SQ Sequence 8 AA;  
XX  
XX Alignment Scores:  
XX Pred. No.: 9.59e+07 Length: 8  
XX Score: 3.00 Matches: 3  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 2 Gaps: 0  
XX  
XX US-10-070-588A-112 (1-11) x AAR73489 (1-8)  
XX  
XX QY 3 TTGGCACTA 11  
XX  
XX DB 2 LeuAlaLeu 4  
XX



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XX PS Claim 26; Page 71; 105pp; English.
XX CC Polypeptides comprising 8-20 amino acids from the HCV E2 region sequence
XX CC in AAR84357 (spanning positions 571-638) and containing a T-cell
XX CC stimulating epitope are used in HCV immunogenic compositions. The present
XX CC sequence is a specifically claimed example of such a T-cell epitope-
XX CC containing region
XX SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR84450 (1-8)

QY 1 CTTTGGGAC 9
DB 1 LeutrPhis 3

RESULT 20
ADC81358
ID ADC81358 standard; peptide; 8 AA.
XX AC ADC81358;
XX AC
XX DT 01-JAN-2004 (first entry)
XX DE Bovin THF-gamma2 analogue V4-THF gamma2.
XX XX
XX KW Cow; thymic humoral factor gamma2; THF-gamma2; concanavalin A;
XX KW Con A-induced interleukin-2 production; mouse spleen cells;
XX KW granulocyte-monocyte colony forming cell; GM-CFC; mouse bone marrow;
XX KW immunomodulatory agent; congenital immune defect;
XX KW primary T cell deficiency; thymic dysplasia; Down's syndrome;
XX KW viral infection; herpes; adenovirus infection; HIV infection;
XX KW subacute sclerosing pan-encephalitis; immune suppression; leukopaenia;
XX KW cancer; chemotherapy; radiotherapy; autoimmune inflammatory disorder;
XX KW rheumatoid arthritis; systemic lupus erythematosus; psoriasis;
XX KW bone marrow transplantation; atopic condition; asthma; atopic dermatitis;
XX KW mutant; mutein.
XX OS Synthetic.
XX OS Bos taurus.
XX PH
XX FT Key Location/Qualifiers
XX FT Misc-difference 4 /note= "Wild-type Gly substituted by Val"
XX FT
XX PN WO9501182-A1.
XX PN
XX PD 12-JAN-1995.
XX XX
XX PF 28-JUN-1994; 94WO-US007304.
XX XX
XX PR 01-JUL-1993; 93IL-00106214.
XX XX
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX XX
XX PI Rycus A, Burstein Y, Trainin N;
XX XX
XX DR WPI; 1995-060814/08.
XX XX
XX PT New thymic humoral factor gamma 2 analogues - used as immunomodulatory
XX PT agents for treating e.g. immune defects, viral infections or autoimmune
XX PT disease.
XX PS Claim 15; Page 25; 30pp; English.

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XX CC A peptide is claimed which is a thymic humoral factor (THF)-gamma2
XX CC analogue of at least 4 amino acid (AA) residues or a functional
XX CC derivative or salt, capable of enhancing concanavalin A (Con A)-induced
XX CC interleukin-2 (IL-2) production in mouse spleen cells and/or the number
XX CC of granulocyte-monocyte colony forming cells (GM-CFC) of mouse bone
XX CC marrow. The peptide comprises one or more sequences corresponding to the
XX CC sequence of the wild-type THF-gamma2 but differing by (i) deletion of one
XX CC or more AA residues, (ii) addition of one or more AA residues at the N-
XX CC and/or C-terminus, (iii) substitution of one or more AA residues by a
XX CC protein natural or non-natural AA residue, (iv) cyclisation through a
XX CC free carboxyl group and a free amino group or through disulphide bonds of
XX CC cysteine residues or (v) linkage of two or more sequences or modified
XX CC sequences corresponding to (i)-(iv), either directly or through a peptide
XX CC or non-peptide chain. The peptides are used as immunomodulatory agents.
XX CC They can be used for treating e.g. congenital immune defects involving
XX CC primary T cell deficiencies such as thymic dysplasia and Down's syndrome,
XX CC primary and secondary viral infections (e.g. herpes virus, adenovirus and
XX CC HIV), as well as subacute infections such as subacute sclerosing pan-
XX CC encephalitis, immune suppression and leukopaenia following cancer
XX CC treatment by chemotherapy and/or radiotherapy, autoimmune inflammatory
XX CC disorders, e.g. rheumatoid arthritis, systemic lupus erythematosus and
XX CC psoriasis, in bone marrow transplantation to prevent viral infections and
XX CC in atopic conditions such as asthma and atopic dermatitis. The present
XX CC sequence is a bovine THF-gamma2 analogue peptide of the invention.
XX SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x ADC81358 (1-8)

QY 9 GTGCCAAG 1
DB 4 ValProlys 6

RESULT 21
AAW36922
ID AAW36922 standard; peptide; 8 AA.
XX AC AAW36922;
XX AC
XX DT 17-MAR-1998 (first entry)
XX DE Peptide epitope 17 of CD47 extracellular domain for the C5/D5 antibody.
XX XX
XX KW CD47 epitope; C5/D5 antibody; colonic epithelial cell; neutrophil; PMN;
XX KW transmigration; immune response modulation; OVTL3; IAP;
XX KW extracellular domain.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO9727873-A1.
XX XX
XX PD 07-AUG-1997.
XX XX
XX PF 28-JAN-1997; 97WO-US001340.
XX XX
XX PR 30-JAN-1996; 96US-00593815.
XX XX
XX PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX XX
XX PI Parkos CA, Madara JL;
XX XX
XX DR WPI; 1997-402315/37.
XX XX
XX PT Monoclonal antibody, C5-D5, and related CD47 epitope(s) - used for

```



PT inhibiting CD47-expressing cell migration, and for modulating immune  
 PS responses.

XX Claim 15; Page 65; 87pp; English.

XX Peptides AAW36906-38 represent CD47 epitopes for the C5/D5 antibody. All  
 CC of the epitopes are found within an N-terminal fragment of CD47, AAW36904  
 CC -5. CD47 is expressed on both colonic epithelial cells, as well as as  
 CC neutrophils (PMN). This suggests that CD47 may be utilised by both  
 CC epithelia and PMN during transmigration of PMN across columnar epithelia  
 CC in vivo. The preferred peptide epitopes are AAW36920 and AAW36934.  
 CC Searches for sequence homology of the epitopes revealed a complete match  
 CC for AAW36937 and AAW36938 with a membrane protein OVTL3 (also known as  
 CC integrin associated protein (IAP)). A novel composition comprises an  
 CC inhibitory agent selected from the C5/D5 antibody, functionally active  
 CC fragments of this antibody, and monoclonal antibodies with the  
 CC characteristics of this antibody. This composition can be used for  
 CC inhibiting the migration of a CD47-expressing cell across a cell layer,  
 CC extracellular matrix or a filter. C5/D5 can also be used for modulating  
 CC an immune response in a subject

XX Sequence 8 AA;

Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW36922 (1-8)

Qy 10 AGTGCCAAA 2  
 Db |||||

2 SerAlaLys 4

RESULT 22

AAW36925

ID AAW36925 standard; peptide; 8 AA.

XX AAW36925;

XX 17-MAR-1998 (first entry)

XX Peptide epitope 20 of CD47 extracellular domain for the C5/D5 antibody.

XX CD47 epitope; C5/D5 antibody; colonic epithelial cell; neutrophil; PMN;  
 KW transmigration; immune response modulation; OVTL3; IAP;  
 KW extracellular domain.

XX Homo sapiens.

XX WO9727873-A1.

XX 07-AUG-1997.

XX 28-JAN-1997; 97WO-US001340.

XX 30-JAN-1996; 96US-00593815.

XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.

XX Parkos CA, Madara JL;

XX WPI; 1997-402315/37.

XX Monoclonal antibody, C5-D5, and related CD47 epitope(s) - used for  
 PT inhibiting CD47-expressing cell migration, and for modulating immune  
 PT responses.

XX Claim 15; Page 67; 87pp; English.

CC Peptides AAW36906-38 represent CD47 epitopes for the C5/D5 antibody. All  
 CC of the epitopes are found within an N-terminal fragment of CD47, AAW36904  
 CC -5. CD47 is expressed on both colonic epithelial cells, as well as as  
 CC neutrophils (PMN). This suggests that CD47 may be utilised by both  
 CC epithelia and PMN during transmigration of PMN across columnar epithelia  
 CC in vivo. The preferred peptide epitopes are AAW36920 and AAW36934.  
 CC Searches for sequence homology of the epitopes revealed a complete match  
 CC for AAW36937 and AAW36938 with a membrane protein OVTL3 (also known as  
 CC integrin associated protein (IAP)). A novel composition comprises an  
 CC inhibitory agent selected from the C5/D5 antibody, functionally active  
 CC fragments of this antibody, and monoclonal antibodies with the  
 CC characteristics of this antibody. This composition can be used for  
 CC inhibiting the migration of a CD47-expressing cell across a cell layer,  
 CC extracellular matrix or a filter. C5/D5 can also be used for modulating  
 CC an immune response in a subject

XX Sequence 8 AA;

Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW36925 (1-8)

Qy 10 AGTGCCAAA 2

Db |||||

4 SerAlaLys 6

RESULT 23

AAW79266

ID AAW79266 standard; peptide; 8 AA.

XX AAW79266;

XX 15-FEB-1999 (first entry)

XX Bovine glucuronyl C5-epimerase N-terminal peptide.

XX Glucuronyl C5-epimerase; cattle; D-glucuronic acid; L-iduronic acid;  
 KW heparin; heparan sulphate.

XX Bos taurus.

XX Key Location/Qualifiers

FT Misc-difference 4 /note= "unidentified residue"

XX WO9848006-A1.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-SE000703.

XX 18-APR-1997; 97SE-00001454.

XX (LIND)/ LINDAHL U.

XX (LIJJ)/ LI J.

XX Lindahl U, Li J;

XX WPI; 1998-583655/49.

XX DNA sequence coding for mammalian glucuronyl C5-epimerase and functional  
 PT derivatives - capable of converting D-glucuronic acid to L-iduronic acid  
 PT in the synthesis of heparin and heparan sulphate.

XX Disclosure; Page 16; 26pp; English.

XX This is an N-terminal peptide of a glucuronyl C5-epimerase purified from

CC bovine liver. It corresponds to amino acid residues 74-86 of the deduced  
 CC amino acid sequence (see AAW79263) of the epimerase. N-terminal and  
 CC internal peptides (see AAW79264-70) of the epimerase were produced by  
 CC digestion of the purified epimerase using a lysine-specific protease. PCR  
 CC primers (see AAV62689-91) based on one of these peptides (see AAW79270)  
 CC were used to generate a probe that was utilised in the isolation of  
 CC glucuronyl C5-epimerase cDNA (see AAV62688) from a bovine lung cDNA  
 CC library. The invention relates to isolated or recombinant DNA sequences  
 CC for a mammalian (including human) glucuronyl C5-epimerase or its  
 CC functional derivative. These can be used for the recombinant production  
 CC of the enzyme, which is useful for converting D-glucuronic acid to L-  
 CC iduronic acid in the biosynthesis of heparin and heparan sulphate  
 XX

SQ Sequence 8 AA;

Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW79266 (1-8)

QY 9 GTGCCAAG 1

DB 6 ValProLys 8

RESULT 24

AAW56853

ID AAW56853 standard; peptide; 8 AA.

XX AC AAW56853;

XX DT 28-JUL-1998 (first entry)

XX DE Enzyme inhibitor peptide SEQ ID NO:54.

XX KW Enzyme inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active;

XX KW latent; substrate subtraction phage display peptide library;

XX KW identification; kinase; phosphatase; serpin.

XX OS Homo sapiens.

XX PN WO9747314-A1.

XX PD 18-DEC-1997.

XX PF 10-JUN-1997; 97WO-US009760.

XX PR 10-JUN-1996; 96US-0019495P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Madison EL, Ke S;

XX DR WPI; 1998-062746/06.

XX PT Substrate subtraction phage display peptide libraries - used to  
 XX distinguish between active and latent forms of enzyme, e.g. serine  
 XX protease.

XX PS Claim 25; Page 58; 138pp; English.

XX CC The present sequence represents an enzyme inhibitor peptide used in the  
 CC method of the invention to distinguish between t-PA and u-PA. The present  
 CC invention describes a substrate subtraction library for the  
 CC identification of peptide substrates selective between a first enzyme  
 CC (E1) and a second enzyme (E2), comprising a collection of different  
 CC peptides, substantially lacking peptides that are effective substrates  
 CC for E1. Also described are: (1) a method (M1) for identifying peptide  
 CC substrates selective between a first enzyme (E1) and a second enzyme (E2)

CC ; (2) a compound comprising the amino acid sequence of a peptide  
 CC identified by M1; (3) a polypeptide for use as an enzyme inhibitor  
 CC comprising one of 237 amino acid sequences (see AAW56801 to AAW56947, and  
 CC AAW56949 to AAW57038); (4) a recombinant DNA vector comprising DNA (I)  
 CC encoding a protease inhibitor including the sequence identified by the M1  
 CC ; (5) a prokaryotic or eukaryotic cell containing the vector of (4); (6)  
 CC an antibody (Ab) immunoreactive with at least one of the peptides  
 CC identified by M1; and (7) a diagnostic assay for distinguishing between  
 CC active and latent forms of protease inhibitors, that uses (Ab). The  
 CC library and method are used for distinguishing between active and latent  
 CC forms of enzyme inhibitors, e.g. proteases, kinases and phosphatases.  
 CC (Ab) are used for affinity purification of recombinant peptides and in  
 CC the identification of naturally occurring protease inhibitors. Enzyme-  
 CC inhibiting peptides identified can be used to treat a serpin deficiency  
 CC or a disorder of serine proteases  
 XX

SQ Sequence 8 AA;

Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW56853 (1-8)

QY 10 AGTGCCAAA 2

DB 4 SerAlaLys 6

RESULT 25

AAW75829

ID AAW75829 standard; peptide; 8 AA.

XX AC AAW75829;

XX DT 27-OCT-1998 (first entry)

XX DE Mouse mast cell protease (mMCP-6) susceptible peptide 23.

XX KW Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;  
 XX KW tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;  
 XX KW anioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;  
 XX KW hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;  
 XX KW inflammatory skin condition.

XX OS Synthetic.

XX OS Mus sp.

XX PN WO9833812-A1.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US001865.

XX PR 05-FEB-1997; 97US-0037090P.

XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX PI Stevens RL, Huang C;

XX DR WPI; 1998-437390/37.

XX PT Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated  
 XX inflammatory disorders e.g. asthma.

XX PS Example; Page 26; 69pp; English.

XX CC Sequences shown in AAW75807 to AAW75835 represent mouse mast cell  
 CC protease (mMCP-6) susceptible peptides obtained in the absence of  
 CC heparin. The invention provides sequences shown in AAW63160 to AAW63169

CC that are inhibitors of mmp-6. These tryptase-6 complex inhibitor  
 CC peptides can be used for treating a mast cell-mediated inflammatory  
 CC disorder. The inhibitors can be used to treat inflammatory disorders  
 CC including asthma, allergic rhinitis, urticaria and atopic dermatitis, eczematous  
 CC dermatitis (atopic dermatitis), hyperproliferative skin disease,  
 CC anaphylaxis, peptic ulcers, inflammatory bowel disorder,  
 CC hyperresponsiveness and inflammatory skin conditions

XX Sequence 8 AA;

Alignment Scores: Length: 8  
 Pred. No.: 9.59e+07  
 Score: 3.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 2

US-10-070-588A-112 (1-11) x AAW75829 (1-8)

Oy 3 TTGGCACTA 11  
 |||||  
 Db 2 LeuAlaLeu 4

RESULT 26

AAAY20315  
 ID AAY20315 standard; protein; 8 AA.

XX AC AAY20315;

XX DT 22-JUL-1999 (first entry)

XX DE Human microtubule associated protein 2 mutant fragment 11.

XX KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9845322-A2.

XX PD 15-OCT-1998.

XX PF 02-APR-1998; 98WO-IB000705.

XX PR 10-APR-1997; 97US-0043163P.

XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

XX PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX PA (UYUT-) RIJKSUNIV UTRECHT.

XX PI Van Leeuwen FW, Grosveld FG, Burbach JPH;

XX WPI; 1998-609901/51.

XX DR N-PSDB; AAX75757.

XX PT Diagnosing disease by detecting frameshift mutations in RNA or  
 PT corresponding protein mutations - used to diagnose cancer and  
 PT neurological diseases, particularly Alzheimer's disease, and also for  
 PT treatment and prevention with specific ribozymes or wild-type RNA.

XX PS Disclosure; Fig 6; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease

CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
 CC proteins tau and Big tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGP-C) and neuroendocrine specific protein A

XX SQ Sequence 8 AA;

Alignment Scores: Length: 8  
 Pred. No.: 9.59e+07  
 Score: 3.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 2

US-10-070-588A-112 (1-11) x AAY20315 (1-8)

Oy 3 TTGGCACTA 11  
 |||||  
 Db 6 LeuAlaLeu 8

RESULT 27

AAW59492  
 ID AAW59492 standard; peptide; 8 AA.

XX AC AAW59492;

XX DT 28-AUG-1998 (first entry)

XX DE Human proinsulin C-peptide fragment #5.

XX KW Insulin; C peptide; proinsulin; Na+K-ATPase activity; biomimetic;  
 KW renal tubule cell; fibroblast; type I diabetes; treatment; nephropathy;  
 KW neuropathy; retinopathy.

XX OS Homo sapiens.

XX PN WO9813384-A1.

XX PD 02-APR-1998.

XX PF 26-SEP-1997; 97WO-GB002627.

XX PR 27-SEP-1996; 96SE-00003533.

XX (CREA-) CREATIVE PEPTIDES SWEDEN AB.  
 XX (DZIE/) DZIEGLEWSKA H E.

XX PI Wahren J, Johansson B, Joernvall H;  
 WPI; 1998-271706/24.

XX DR Human insulin C peptide(s) - stimulate sodium potassium ATPase activity,  
 XX useful for combating diabetes and related complications.

XX PS Disclosure; Page 38; 49pp; English.

XX AAW59482-W59494 are fragments of the human insulin C peptide which are  
 CC used to stimulate Na+K-ATPase activity. These fragments can be used to  
 CC produce a biomimetic organic compound that stimulates Na+K-ATPase

CC activity and which binds to renal tubule cells and fibroblasts and/or  
 CC cellular binding characteristics. The peptides and biomimetic compounds  
 CC are used to combat diabetes or diabetic complications, or to stimulate  
 CC Na-K-ATPase activity in a human or non-human subject. They may be  
 CC administered alone or in conjunction with another active agent, e.g.  
 CC insulin. When administered with insulin the compositions can be used to  
 CC treat type 1 diabetes, optionally with nephropathy, neuropathy or  
 CC retinopathy or they can be used for retarding the development of late  
 CC diabetic complications  
 XX Sequence 8 AA;

Alignment Scores:                      9.59e+07                      Length:                      8  
 Pred. No.:                      3.00                      Matches:                      3  
 Score:                      100.00%                      Conservative:                      0  
 Percent Similarity:                      100.00%                      Mismatches:                      0  
 Best Local Similarity:                      100.00%                      Indels:                      0  
 Query Match:                      2                      Gaps:                      0  
 DB:

US-10-070-588A-112 (1-11) x AAW59492 (1-8)

Qy    3 TTGGCACTA 11  
 Db    1 LeuAlaLeu 3

RESULT 28

AAW78686

ID    AAW78686 standard; peptide; 8 AA.

XX    AC    AAW78686;

DT    04-NOV-1998    (first entry)

DE    SH2 domain binding inhibiting peptide SEQ ID NO:181.

XX    SH2 domain; binding; inhibition; interaction; site specific;  
 KW    signal transduction; protein tyrosine kinase; phosphotyrosine;  
 KW    growth factor receptor; oncogene; cellular growth; cell proliferation;  
 KW    metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.

XX    Synthetic.

XX    Key                      Location/Qualifiers  
 FH    Misc-difference 1  
 FT    Misc-difference 8 /note= "unspecified"  
 FT    Misc-difference 8 /note= "unspecified"

XX    US5801149-A.

XX    01-SEP-1998.

XX    21-MAR-1995;    95US-00408604.

XX    19-JUN-1991;    91US-00722359.

XX    09-OCT-1992;    92US-00959949.

XX    08-OCT-1993;    93US-00134558.

XX    (JOSL-) JOSLIN DIABETES CENT INC.

XX    Shoelson S;

XX    WPI; 1998-494822/42.

XX    Inhibiting site-specific SH2 domain interaction - with peptide containing  
 FT    phosphotyrosine or phosphotyrosine mimic.

XX    Disclosure; Col 109; 70pp; English.

CC    A method has been developed of inhibiting a site-specific interaction  
 CC    between a first molecule having an SH2 domain and a second molecule that  
 CC    interacts with the SH2 domain. The method comprises contacting the first

CC molecule with a 4- to 30-mer peptide containing a sequence of formula: R1  
 CC -Met-R3-Met (1), where R1 = phosphotyrosine (pTyr) or a phosphotyrosine  
 CC analogue having a hydrolysis-resistant phosphorous moiety, and R3 = any  
 CC amino acid. AAW78501 to AAW78523 represent specifically claimed examples  
 CC of the peptides described. The peptides are useful for modulating both  
 CC cellular growth to control unwanted cell proliferation in e.g. selected  
 CC malignancies and for metabolic control in e.g. diabetes, by inhibiting  
 CC signal transduction molecules such as protein tyrosine kinases (PTKs)  
 CC which include growth factor receptors, proto-oncogene and oncogene  
 CC products and the insulin receptor. The peptides are also useful for  
 CC treating and for studying the enzymatic mechanisms of PTPase activity and  
 CC the metabolic and biochemical roles of PTPases. AAW78524 to AAW78702  
 CC represent other peptides given in the present invention, but which are  
 CC not specifically claimed

SQ    Sequence 8 AA;

Alignment Scores:                      9.59e+07                      Length:                      8  
 Pred. No.:                      3.00                      Matches:                      3  
 Score:                      100.00%                      Conservative:                      0  
 Percent Similarity:                      100.00%                      Mismatches:                      0  
 Best Local Similarity:                      100.00%                      Indels:                      0  
 Query Match:                      2                      Gaps:                      0  
 DB:

US-10-070-588A-112 (1-11) x AAW78686 (1-8)

Qy    10 AGTGCCAAA 2

Db    5 SerAlaLys 7

RESULT 29

AAW78521

ID    AAW78521 standard; peptide; 8 AA.

XX    AC    AAW78521;

XX    04-NOV-1998    (first entry)

DE    SH2 domain binding inhibiting peptide SEQ ID NO:207.

XX    SH2 domain; binding; inhibition; interaction; site specific;  
 KW    signal transduction; protein tyrosine kinase; phosphotyrosine;  
 KW    growth factor receptor; oncogene; cellular growth; cell proliferation;  
 KW    metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.

XX    Synthetic.

XX    Key                      Location/Qualifiers  
 FH    Modified-site 1  
 FT    /note= "acetylated phosphotyrosine"

XX    US5801149-A.

XX    01-SEP-1998.

XX    21-MAR-1995;    95US-00408604.

XX    19-JUN-1991;    91US-00722359.

XX    09-OCT-1992;    92US-00959949.

XX    08-OCT-1993;    93US-00134558.

XX    (JOSL-) JOSLIN DIABETES CENT INC.

XX    Shoelson S;

XX    WPI; 1998-494822/42.

XX    Inhibiting site-specific SH2 domain interaction - with peptide containing  
 FT    phosphotyrosine or phosphotyrosine mimic.

XX    Claim 16; Col 125-126; 70pp; English.

CC A method has been developed of inhibiting a site-specific interaction  
CC between a first molecule having an SH2 domain and a second molecule that  
CC interacts with the SH2 domain. The method comprises contacting the first  
CC molecule with a 4- to 30-mer peptide containing a sequence of formula: R1  
CC -Met-R3-Met (1), where R1 = phosphotyrosine (pTyr) or a phosphotyrosine  
CC analogue having a hydrolysis-resistant phosphorous moiety, and R3 = any  
CC amino acid. AAW78501 to AAW78523 represent specifically claimed examples  
CC of the peptides described. The peptides are useful for modulating both  
CC cellular growth to control unwanted cell proliferation in e.g. selected  
CC malignancies and for metabolic control in e.g. diabetes, by inhibiting  
CC signal transduction molecules such as protein tyrosine kinases (PTKs)  
CC which include growth factor receptors, proto-oncogene and oncogene  
CC products and the insulin receptor. The peptides are also useful for  
CC treating and for studying the enzymatic mechanisms of PTPase activity and  
CC the metabolic and biochemical roles of PTPases. AAW78524 to AAW78702  
CC represent other peptides given in the present invention, but which are  
CC not specifically claimed

XX Sequence 8 AA;

Alignment Scores:  
Pred. No.: 9.59e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW78521 (1-8)

Qy 10 AGTGCCAAA 2  
Db 5 SerAlalays 7

AAW67227  
ID AAW67227 standard; peptide; 8 AA.

AC AAW67227;

XX 18-DEC-1998 (first entry)

XX aPL immunoreactive peptide derivative #77.

XX antiphospholipid; aPL; analogue; stroke; foetal loss; B cell; epitope;  
XX thrombosis; antibody ACA-6641; conjugate; phage library screen;  
XX biopanning; micropanning.

XX Synthetic.

XX Key Location/Qualifiers  
XX Modified-site 1 /note= "homocysteine"

XX WO9746251-A1.

XX 11-DEC-1997.

XX 06-JUN-1997; 97WO-US010075.

XX 06-JUN-1996; 96US-00660092.

XX 05-DEC-1996; 96US-00760508.

XX (LJOL-) LA JOLLA PHARM CO.

XX Victoria EJ, Marquis DM, Jones DS, Yu L;

XX WPI, 1998-051902/05.

XX New anti-phospholipid analogues and conjugates containing them - are  
XX useful in treatment of disorders mediated by antiphospholipid antibody,  
XX such as stroke or foetal loss.

XX

PS Disclosure; Page 38; 155pp; English.

XX The invention relates to antiphospholipid (aPL) analogues that bind  
CC specifically to B cells to which an aPL epitope binds. Optimised  
CC analogues lack T cell epitope(s) and are useful as conjugates for  
CC treating aPL antibody-mediated diseases. Conjugates comprising aPL  
CC analogues and non-immunogenic valency platform molecules are provided as  
CC are novel non-immunogenic valency platform molecules and linkers. Methods  
CC of preparing and identifying the analogues, methods of treatment and  
CC methods and compositions for preparing conjugates of the analogues and  
CC diagnostic immunoassays for aPL antibodies are disclosed. The conjugates  
CC are useful for treatment of aPL antibody-mediated diseases, such as  
CC stroke, foetal loss, antiphospholipid antibody syndrome or thrombosis.  
CC Peptide 6641/3G3 (AAW67144) was isolated from a phage library screen  
CC using aPL antibody ACA-6641. This peptide was subjected to a number of  
CC analyses, including truncation at both the N-terminus and C-terminus,  
CC disulphide substitution, substitution of alanine and glycine for amino  
CC acids in positions 2 through 8 etc. The present sequence represents one  
CC of these substitutions or truncations. The structure/activity  
CC relationship of these substitutions or truncations was determined

XX Sequence 8 AA;

Alignment Scores:  
Pred. No.: 9.59e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW67227 (1-8)

Qy 3 TTGGCACTA 11  
Db 5 LeuAlaleu 7

RESULT 31

AAW67141

ID AAW67141 standard; peptide; 8 AA.

AC AAW67141;

XX 18-DEC-1998 (first entry)

XX Antibody ACA-6644 epitope isolated from a phage library screen.

XX antiphospholipid; aPL; analogue; stroke; foetal loss; B cell; epitope;  
XX thrombosis; antibody ACA-6501; conjugate; phage library screen;  
XX biopanning; micropanning.

XX Synthetic.

XX WO9746251-A1.

XX 11-DEC-1997.

XX 06-JUN-1997; 97WO-US010075.

XX 06-JUN-1996; 96US-00660092.

XX 05-DEC-1996; 96US-00760508.

XX (LJOL-) LA JOLLA PHARM CO.

XX Victoria EJ, Marquis DM, Jones DS, Yu L;

XX WPI, 1998-051902/05.

XX New anti-phospholipid analogues and conjugates containing them - are  
XX useful in treatment of disorders mediated by antiphospholipid antibody,  
XX such as stroke or foetal loss.

XX Disclosure; Page 27; 155pp; English.

XX The invention relates to antiphospholipid (aPL) analogues that bind  
 CC specifically to B cells to which an aPL epitope binds. Optimised  
 CC analogues lack T cell epitope(s) and are useful as conjugates for  
 CC treating aPL antibody-mediated diseases. Conjugates comprising aPL  
 CC analogues and non-immunogenic valency platform molecules are provided as  
 CC are novel non-immunogenic valency platform molecules and linkers. Methods  
 CC of preparing and identifying the analogues, methods of treatment and  
 CC methods and compositions for preparing conjugates of the analogues and  
 CC diagnostic immunoassays for aPL antibodies are disclosed. The conjugates  
 CC are useful for treatment of aPL antibody-mediated diseases, such as  
 CC stroke, foetal loss, antiphospholipid antibody syndrome or thrombosis.  
 CC The present sequence represents an epitope that was isolated from a phage  
 CC library screen using aPL antibody ACA-6644

XX Sequence 8 AA;

Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW67141 (1-8)

Qy 3 TTGGCACTA 11  
 Db 3 LeuAlaLeu 5

RESULT 32

AAW29699  
 ID AAW29699 standard; peptide; 8 AA.

XX AAW29699;

XX 26-OCT-1998 (first entry)

XX TNF receptor releasing enzyme (TRRE), internal sequence 15.

XX Tumour necrosis factor; TNF; inflammation; autoimmune disease; diabetes;  
 KW rheumatoid arthritis; multiple sclerosis; cancer; glioblastoma; melanoma;  
 KW neuroblastoma; carcinoma; adenocarcinoma; soft tissue sarcoma; leukaemia;  
 KW lymphoma; antibody; enzyme.

XX Synthetic.  
 OS Homo sapiens.

XX WO9820140-A1.

XX 14-MAY-1998.

XX 05-NOV-1997; 97WO-US019930.

XX 06-NOV-1996; 96US-0030761P.

XX (REGC ) UNIV CALIFORNIA.

XX Granger GA, Gatanaga T;

XX WPI; 1998-286955/25.

XX New enzymes that release soluble tumour necrosis factor receptor and  
 PT related antibodies - for treatment of inflammation etc., also use of  
 PT their inhibitors for treatment of cancer, and diagnosis based on  
 PT detecting elevated levels of the enzyme.

XX Claim 8; Page 80; 109pp; English.

XX Sequences AAW29684-W296714 are internal sequences of the TNF receptor  
 CC releasing enzyme, which can be used to treat diseases associated with  
 CC altered levels of TNF activity, particularly inflammatory diseases and

CC autoimmune diseases e.g. diabetes, rheumatoid arthritis, multiple  
 CC sclerosis. Measurement of the TNF receptor releasing enzyme levels can  
 CC also be used to diagnose diseases, particularly cancer, e.g.  
 CC glioblastoma, melanoma, neuroblastoma, carcinoma, adenocarcinoma, soft  
 CC tissue sarcoma, leukaemia and lymphoma. These diseases can be treated  
 CC with antibodies that target this enzyme, which will increase the level of  
 CC TNF at the site of disease, and may also be administered to subjects at  
 CC risk of tumour recurrence

XX Sequence 8 AA;

Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW29699 (1-8)

Qy 3 TTGGCACTA 11  
 Db 1 LeuAlaLeu 3

RESULT 33

AAW29698  
 ID AAW29698 standard; peptide; 8 AA.

XX AAW29698;

XX 26-OCT-1998 (first entry)

XX TNF receptor releasing enzyme (TRRE), internal sequence 14.

XX Tumour necrosis factor; TNF; inflammation; autoimmune disease; diabetes;  
 KW rheumatoid arthritis; multiple sclerosis; cancer; glioblastoma; melanoma;  
 KW neuroblastoma; carcinoma; adenocarcinoma; soft tissue sarcoma; leukaemia;  
 KW lymphoma; antibody; enzyme.

XX Synthetic.

OS Homo sapiens.

XX WO9820140-A1.

XX 14-MAY-1998.

XX 05-NOV-1997; 97WO-US019930.

XX 06-NOV-1996; 96US-0030761P.

XX (REGC ) UNIV CALIFORNIA.

XX Granger GA, Gatanaga T;

XX WPI; 1998-286955/25.

XX New enzymes that release soluble tumour necrosis factor receptor and  
 PT related antibodies - for treatment of inflammation etc., also use of  
 PT their inhibitors for treatment of cancer, and diagnosis based on  
 PT detecting elevated levels of the enzyme.

XX Claim 8; Page 80; 109pp; English.

XX Sequences AAW29684-W296714 are internal sequences of the TNF receptor  
 CC releasing enzyme, which can be used to treat diseases associated with  
 CC altered levels of TNF activity, particularly inflammatory diseases and  
 CC autoimmune diseases e.g. diabetes, rheumatoid arthritis, multiple  
 CC sclerosis. Measurement of the TNF receptor releasing enzyme levels can  
 CC also be used to diagnose diseases, particularly cancer, e.g.

CC glioblastoma, melanoma, neuroblastoma, carcinoma, adenocarcinoma, soft  
 CC tissue sarcoma, leukaemia and lymphoma. These diseases can be treated  
 CC with antibodies that target this enzyme, which will increase the level of

CC TNF at the site of disease, and may also be administered to subjects at  
 CC risk of tumour recurrence

SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW29698 (1-8)

OY 3 TTGGCACTA 11  
 |||||  
 Db 1 LeuAlaLeu 3

RESULT 34

AAW29700  
 ID AAW29700 standard; peptide; 8 AA.

XX AAW29700;

DT 26-OCT-1998 (first entry)

DE TNF receptor releasing enzyme (TRRE), internal sequence 16.

XX Tumour necrosis factor; TNF; inflammation; autoimmune disease; diabetes;  
 KW rheumatoid arthritis; multiple sclerosis; cancer; glioblastoma; melanoma;  
 KW neuroblastoma; carcinoma; adenocarcinoma; soft tissue sarcoma; leukaemia;  
 KW lymphoma; antibody; enzyme.

OS Synthetic.

OS Homo sapiens.

PN WO9820140-A1.

PD 14-MAY-1998.

PF 05-NOV-1997; 97WO-US019930.

PR 06-NOV-1996; 96US-0030761P.

PA (REGC ) UNIV CALIFORNIA.

PI Granger GA, Gatanaga T;

DR WPI; 1998-286955/25.

XX New enzymes that release soluble tumour necrosis factor receptor and  
 PT related antibodies - for treatment of inflammation etc., also use of  
 PT their inhibitors for treatment of cancer, and diagnosis based on  
 PT detecting elevated levels of the enzyme.

PS Claim 8; Page 80; 109pp; English.

XX Sequences AAW29684-W296714 are internal sequences of the TNF receptor  
 CC releasing enzyme, which can be used to treat diseases associated with  
 CC altered levels of TNF activity, particularly inflammatory diseases and  
 CC autoimmune diseases e.g. diabetes, rheumatoid arthritis, multiple  
 CC sclerosis. Measurement of the TNF receptor releasing enzyme levels can  
 CC also be used to diagnose diseases, particularly cancer, e.g.  
 CC glioblastoma, melanoma, neuroblastoma, carcinoma, adenocarcinoma, soft  
 CC tissue sarcoma, leukaemia and lymphoma. These diseases can be treated  
 CC with antibodies that target this enzyme, which will increase the level of  
 CC TNF at the site of disease, and may also be administered to subjects at  
 CC risk of tumour recurrence

SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW29700 (1-8)

OY 3 TTGGCACTA 11  
 |||||  
 Db 1 LeuAlaLeu 3

RESULT 35

AAW29697  
 ID AAW29697 standard; peptide; 8 AA.

XX AAW29697;

DT 26-OCT-1998 (first entry)

DE TNF receptor releasing enzyme (TRRE), internal sequence 13.

XX Tumour necrosis factor; TNF; inflammation; autoimmune disease; diabetes;  
 KW rheumatoid arthritis; multiple sclerosis; cancer; glioblastoma; melanoma;  
 KW neuroblastoma; carcinoma; adenocarcinoma; soft tissue sarcoma; leukaemia;  
 KW lymphoma; antibody; enzyme.

OS Synthetic.

OS Homo sapiens.

PN WO9820140-A1.

PD 14-MAY-1998.

PF 05-NOV-1997; 97WO-US019930.

PR 06-NOV-1996; 96US-0030761P.

PA (REGC ) UNIV CALIFORNIA.

PI Granger GA, Gatanaga T;

DR WPI; 1998-286955/25.

XX New enzymes that release soluble tumour necrosis factor receptor and  
 PT related antibodies - for treatment of inflammation etc., also use of  
 PT their inhibitors for treatment of cancer, and diagnosis based on  
 PT detecting elevated levels of the enzyme.

PS Claim 8; Page 80; 109pp; English.

XX Sequences AAW29684-W296714 are internal sequences of the TNF receptor  
 CC releasing enzyme, which can be used to treat diseases associated with  
 CC altered levels of TNF activity, particularly inflammatory diseases and  
 CC autoimmune diseases e.g. diabetes, rheumatoid arthritis, multiple  
 CC sclerosis. Measurement of the TNF receptor releasing enzyme levels can  
 CC also be used to diagnose diseases, particularly cancer, e.g.  
 CC glioblastoma, melanoma, neuroblastoma, carcinoma, adenocarcinoma, soft  
 CC tissue sarcoma, leukaemia and lymphoma. These diseases can be treated  
 CC with antibodies that target this enzyme, which will increase the level of  
 CC TNF at the site of disease, and may also be administered to subjects at  
 CC risk of tumour recurrence

SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW29697 (1-8)

QY 3 TTGGCACTA 11  
Db 1 LeuAlaLeu 3

## RESULT 36

AAW47925  
ID AAW47925 standard; peptide; 8 AA.

XX AC AAW47925;

DT 12-JUN-1998 (first entry)

DE Human MHC class II allele antigenic peptide SEQ ID NO:163.

XX Mammalian II key peptide; mammalian invariant chain protein; allergy;  
KW immune response; MHC class II; antigenic; autoimmune disease.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Acetylated"

FT Modified-site 8

FT /note= "Amidated"

XX PN WO9749430-Al.

XX PD 31-DEC-1997.

XX PF 09-JUN-1997; 97WO-US009993.

XX PR 26-JUN-1996; 96US-00670605.

XX PA (ANTI-) ANTIGEN EXPRESS INC.

XX PI Humphreys RE, Adams S, Xu M;

DR WPI; 1998-076917/07.

XX New mammalian invariant chain protein (Ii) key peptide(s) - used for  
PT modulation of immune response, e.g. for treating malignant, allergic or  
PT autoimmune disease or allograft rejection.

PS Claim 26; Page 142; 149pp; English.

XX The present sequence represents an MHC class II allele antigenic peptide.  
CC The present invention describes a mammalian invariant chain protein (Ii)  
CC key peptide of sequence LRMKLPPKPVSKMR and modifications with the  
CC exclusion of peptide YRMKLPPKPVSKMR. MHC class II molecules are  
CC synthesised in the endoplasmic reticulum with their antigenic peptide  
CC sites blocked by the invariant chain protein (Ii). The products and  
CC method can be used for the modulation of an immune response for  
CC therapeutic or diagnostic purposes. The enhancement of immunity can be  
CC used in the treatment of e.g. malignant or allergic disease. The  
CC immunosuppression can be used for the treatment of autoimmune disease,  
CC e.g. rheumatoid arthritis, multiple sclerosis, diabetes mellitus, lupus  
CC erythematosus, and psoriasis or allograft rejection

XX Sequence 8 AA;

## Alignment Scores:

Pred. No.: 9.59e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW47925 (1-8)

QY 10 AGTGCCAAA 2  
Db 4 SerAlaLys 6

## RESULT 37

AAW67654

ID AAW67654 standard; peptide; 8 AA.

XX AC AAW67654;

DT 16-MAR-1999 (first entry)

DE LXXLL signature motif #4 from protein RIP140.

XX Nuclear protein; signature motif; receptor protein; inflammation; cancer;  
KW interaction; inhibitor; inhibition; transcription factor; ligand.

XX OS Homo sapiens.

XX PN WO9849561-Al.

XX PD 05-NOV-1998.

XX PF 28-APR-1998; 98WO-GB001238.

XX PR 30-APR-1997; 97GB-00008676.

XX PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

XX PI Heery DM, Parker MG;

DR WPI; 1999-034672/03.

XX Identification of inhibitors of nuclear protein/nuclear receptor  
PT interaction - useful for, e.g. treatment of disease mediated through the  
PT interaction such as inflammation and cancer.

PS Example 1; Fig 1A; 60pp; English.

XX This sequence represents an LXXLL nuclear protein signature motif found  
CC in the 140 kD receptor interacting protein (RIP140) from nuclei. This  
CC peptide corresponds to amino acids 266-273 of RIP140. The invention  
CC relates to the identification of inhibitor compounds capable of reducing  
CC the interaction between a region on a nuclear protein (R1) and a region  
CC on a nuclear receptor (R2), where: (i) R1 is a signature motif; (ii) R2  
CC is the region capable of interacting with the nuclear protein by binding  
CC the signature motif; (iii) the nuclear protein is a bridging factor  
CC responsible for interaction between a liganded nuclear receptor and a  
CC transcription initiation complex involved in gene expression regulation;  
CC (iv) the nuclear receptor is a transcription factor; (v) the signature  
CC motif is a short amino acid sequence which is the key structural element  
CC of a nuclear protein which binds to a liganded nuclear receptor during  
CC activation or repression of target genes. The inhibitors are expected to  
CC be useful in the treatment of any disease mediated through any  
CC interaction between a signature motif on a nuclear protein and a nuclear  
CC receptor, for example inflammation and cancer

XX Sequence 8 AA;

## Alignment Scores:

Pred. No.: 9.59e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW67654 (1-8)

QY 3 TTGGCACTA 11

Db 2 LeuAlaLeu 4



```
RESULT 38
AAV16865
ID AAV16865 standard; peptide; 8 AA.
XX
XX AC AAV16865;
XX
XX DT 20-JUL-1999 (first entry)
XX
XX DE Heat shock protein (hsp) binding peptide.
XX
XX KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
XX surface protein; tethering peptide; chaperone process; cytokine; cancer;
XX KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
XX KW acquired immune deficiency; autoimmune disease.
XX
XX OS Synthetic.
XX
XX PN WO9922761-A1.
XX
XX PD 14-MAY-1999.
XX
XX PF 22-OCT-1998; 98WO-US022335.
XX
XX PR 31-OCT-1997; 97US-00961707.
XX
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX PI Rothman JE, Mayhew M, Hoe MH, Houghton A, Hartl U, Querfelli O;
XX PI Moroi Y;
XX
XX DR WPI; 1999-313177/26.
XX DR N-PSDB; AAX60765.
XX
XX PT Identifying peptides which bind heat shock proteins.
XX
XX PS Disclosure; Fig 2H; 155pp; English.
XX
XX CC The invention relates to conjugate peptides engineered to noncovalently
XX bind to heat shock proteins (hsp). A method of identifying a hsp binding
XX peptide comprises (a) contacting a phage display library having
XX bacteriophage expressing, in a surface protein, inserted peptides with a
XX hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a
XX physiologic binding buffer; (b) isolating a phage binding to the hsp
XX target; and (c) identifying the inserted peptide expressed. The peptides
XX which bind to a hsp can be used as tethering peptides for a hsp which may
XX serve as an accessory in a chaperone process and/or may comprise a
XX cytokine. They can also be coupled to antigens to induce an immune
XX response. Such compositions can be used for treating neoplastic disease,
XX e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
XX virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
XX disease of the immune system, e.g. acquired immune deficiencies or
XX autoimmune diseases
XX
XX SQ Sequence 8 AA;
XX
XX Alignment Scores:
XX Pred. No.: 9.59e+07 Length: 8
XX Score: 3.00 Matches: 3
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-10-070-588A-112 (1-11) x AAV16865 (1-8)
XX
XX QY 3 TTGGCACTA 11
XX |||||
XX Db 3 LeuAlaLeu 5
XX
XX RESULT 40
XX AAV93856
XX ID AAV93856 standard; protein; 8 AA.
XX
XX AC AAV93856;
XX
XX DT 25-JUN-1999 (first entry)
XX
```

```
RESULT 39
AAV16846
ID AAV16846 standard; peptide; 8 AA.
XX
XX AC AAV16846;
XX
XX DT 20-JUL-1999 (first entry)
XX
XX DE Heat shock protein (hsp) binding peptide.
XX
XX KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
XX surface protein; tethering peptide; chaperone process; cytokine; cancer;
XX KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
XX KW acquired immune deficiency; autoimmune disease.
XX
XX OS Synthetic.
XX
XX PN WO9922761-A1.
XX
XX PD 14-MAY-1999.
XX
XX PF 22-OCT-1998; 98WO-US022335.
XX
XX PR 31-OCT-1997; 97US-00961707.
XX
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX PI Rothman JE, Mayhew M, Hoe MH, Houghton A, Hartl U, Querfelli O;
XX PI Moroi Y;
XX
XX DR WPI; 1999-313177/26.
XX DR N-PSDB; AAX60746.
XX
XX PT Identifying peptides which bind heat shock proteins.
XX
XX PS Disclosure; Fig 2H; 155pp; English.
XX
XX CC The invention relates to conjugate peptides engineered to noncovalently
XX bind to heat shock proteins (hsp). A method of identifying a hsp binding
XX peptide comprises (a) contacting a phage display library having
XX bacteriophage expressing, in a surface protein, inserted peptides with a
XX hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a
XX physiologic binding buffer; (b) isolating a phage binding to the hsp
XX target; and (c) identifying the inserted peptide expressed. The peptides
XX which bind to a hsp can be used as tethering peptides for a hsp which may
XX serve as an accessory in a chaperone process and/or may comprise a
XX cytokine. They can also be coupled to antigens to induce an immune
XX response. Such compositions can be used for treating neoplastic disease,
XX e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
XX virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
XX disease of the immune system, e.g. acquired immune deficiencies or
XX autoimmune diseases
XX
XX SQ Sequence 8 AA;
XX
XX Alignment Scores:
XX Pred. No.: 9.59e+07 Length: 8
XX Score: 3.00 Matches: 3
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-10-070-588A-112 (1-11) x AAV16846 (1-8)
XX
XX QY 3 TTGGCACTA 11
XX |||||
XX Db 3 LeuAlaLeu 5
XX
XX RESULT 40
XX AAV93856
XX ID AAV93856 standard; protein; 8 AA.
XX
XX AC AAV93856;
XX
XX DT 25-JUN-1999 (first entry)
XX
```

XX Mouse BR96 receptor light chain CDR L1 variant M131B3-12 protein.  
 XX CDR L1; complementarity determining region; receptor; antibody receptor;  
 KW BR96; light chain; optimal binding ligand; drug; diagnostic agent.  
 XX Synthetic.  
 OS Mus sp.  
 XX WO9919506-A2.  
 XX 22-APR-1999.  
 XX 08-OCT-1998; 98WO-US021390.  
 XX 09-OCT-1997; 97US-00948187.  
 PR 09-OCT-1997; 97US-0112011P.  
 XX (IXSY-) IXSYS INC.  
 PA Huse WD, Freedman MH;  
 PI WPI; 1999-277653/23.  
 DR N-PSDB; AAX23892.  
 XX Detecting binding between ligand and receptor using collective variants.  
 XX Example V; Page 53; 70pp; English.  
 PS This invention describes a method which identifies optimal binding  
 CC ligands to a receptor. The method involves the binding of receptor (R) to  
 CC one or more ligands (L), or of an L to one or more R (or its variants),  
 CC and is detected by treating a collective R variant (or L variant) and  
 CC population with one or more L (or R). The method is used to identify L or  
 CC R with optimal binding affinity for a specific target, i.e. potential  
 CC drugs and diagnostic agents, or lead compounds for development of  
 CC variants with increased binding activity. The method identifies the  
 CC optimum binding agent rapidly and efficiently. Using a variant population  
 CC for the initial screen increases the chance of detecting a binding event  
 CC and quickly provides an enriched population with favourable binding  
 CC properties at the target (even those of low affinity for a parent  
 CC receptor). Very many different L may be screened with a single variant R  
 CC population. The method does not require segregation of the receptor  
 CC population, but uses a non-segmented pool, significantly reducing the  
 CC contact area/volume needed and thus increasing screening capacity  
 XX  
 SQ Sequence 8 AA;

Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW93856 (1-8)

QY 10 AGTGCCAAA 2  
 DB 3 SerAlaLys 5

RESULT 41  
 AAB28324  
 ID AAB28324 standard; peptide; 8 AA.  
 XX AC AAB28324;  
 XX 14-FEB-2001 (first entry)  
 DT Human secreted peptide #29 encoded by cDNA#48.  
 DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW

KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.  
 XX Homo sapiens.  
 OS WO200058355-A1.  
 PN 05-OCT-2000.  
 XX 22-MAR-2000; 2000WO-US007527.  
 XX 26-MAR-1999; 99US-0126501P.  
 PR 22-DEC-1999; 99US-0171551P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Ruben SM, Komatsoulis G;  
 PI WPI; 2000-602358/57.  
 DR N-PSDB; AAC67678.  
 XX Nucleic acid molecules encoding human secreted proteins, used in  
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
 PT Parkinson's diseases and cancers.  
 XX Claim 11; Page 356; 367pp; English.  
 PS Sequences AAB28278-B28326 represent the amino acid sequences of 50 human  
 CC secreted proteins encoded by the genes AAC67631-C67680. The genes and  
 CC proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
 CC a range of human tissues disclosed in the specification. The nucleic  
 CC acids, proteins, antibodies and (ant)agonists are useful in the  
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)  
 CC immune disorders e.g. Addison's disease, diabetes mellitus, Crohn's disease,  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease;  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections  
 XX  
 SQ Sequence 8 AA;

Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAB28324 (1-8)

QY 3 TTGGCACTA 11  
 DB 6 LeuAlaLeu 8

RESULT 42  
 AAY69116  
 ID AAY69116 standard; peptide; 8 AA.  
 XX AC AAY69116;  
 XX 30-MAY-2000 (first entry)  
 DT Subsequence which is capable of being digested by a metalloproteinase.  
 DE Tropoelastin; derivative; proteolysis; protease; antiwrinkle;  
 KW

KW hand lotion; bulking agent; chemotaxis; proliferation; metalloproteinase;  
 KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;  
 KW metastasis; blood clotting.

OS Homo sapiens.

PN WO200004043-A1.

PD 27-JAN-2000.

PP 19-JUL-1999; 99WO-AU000580.

PR 17-JUL-1998; 98AU-00004723.

PA (UNSY ) UNIV SYDNEY.

PI Weiss AS;

PP WPI; 2000-182399/16.

DR New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.

PS Claim 68; Page 127; 136pp; English.

XX The present sequence represents a subsequence which is capable of being  
 CC digested by a metalloproteinase. This sequence can be inserted into human  
 CC tropoelastin to produce the tropoelastin derivatives of the invention,  
 CC which have enhanced susceptibility to protease cleavage. The  
 CC specification describes human tropoelastin derivatives, in which a  
 CC subsequence has been mutated so that susceptibility to proteolysis is  
 CC reduced or eliminated, or a subsequence has been inserted so that  
 CC susceptibility to proteolysis is increased. The derivatives have with  
 CC reduced susceptibility, and can be used where the wild-type protein would  
 CC be degraded too easily, e.g. in contact with serum or wound exudate. The  
 CC tropoelastin derivatives provide competitive inhibition of protease  
 CC activity. The tropoelastin derivatives, and other polypeptides containing  
 CC tropoelastin derivative-derived protease-susceptibility sites, are useful  
 CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand  
 CC lotions), as bulking agents and for inducing chemotaxis. They are also  
 CC useful for proliferation or growth inhibition, particularly of smooth  
 CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,  
 CC chondrocytes and platelets. Peptidomimetics that mimic the protease  
 CC cleavage site in tropoelastin derivatives are competitive inhibitors of  
 CC the protease, and are used for protecting against lung damage caused by  
 CC elastin, for inhibiting or controlling localized growth of cancers or  
 CC metastases, or to limit protease activity that causes blood clotting

SQ Sequence 8 AA;

Alignment Scores:  
 Pred. NO.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAY69116 (1-8)

QY 3 TTGGCACTA 11

DB 3 LeuAlaLeu 5

RESULT 43

RAY69128

ID AAY69128 standard; peptide; 8 AA.

XX AC AAY69128;

XX 30-MAY-2000 (first entry)

DE Subsequence which is capable of being digested by a metalloproteinase.

XX

KW Tropoelastin; derivative; proteolysis; protease; antiwrinkle;

KW hand lotion; bulking agent; chemotaxis; proliferation; metalloproteinase;

KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;

KW metastasis; blood clotting.

OS Homo sapiens.

PN WO200004043-A1.

PD 27-JAN-2000.

PP 19-JUL-1999; 99WO-AU000580.

PR 17-JUL-1998; 98AU-00004723.

PA (UNSY ) UNIV SYDNEY.

PI Weiss AS;

PP WPI; 2000-182399/16.

DR New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and  
 PT cell growth.

PS Claim 68; Page 129; 136pp; English.

XX The present sequence represents a subsequence which is capable of being  
 CC digested by a metalloproteinase. This sequence can be inserted into human  
 CC tropoelastin to produce the tropoelastin derivatives of the invention,  
 CC which have enhanced susceptibility to protease cleavage. The  
 CC specification describes human tropoelastin derivatives, in which a  
 CC subsequence has been mutated so that susceptibility to proteolysis is  
 CC reduced or eliminated, or a subsequence has been inserted so that  
 CC susceptibility to proteolysis is increased. The derivatives have with  
 CC reduced susceptibility, and can be used where the wild-type protein would  
 CC be degraded too easily, e.g. in contact with serum or wound exudate. The  
 CC tropoelastin derivatives provide competitive inhibition of protease  
 CC activity. The tropoelastin derivatives, and other polypeptides containing  
 CC tropoelastin derivative-derived protease-susceptibility sites, are useful  
 CC in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand  
 CC lotions), as bulking agents and for inducing chemotaxis. They are also  
 CC useful for proliferation or growth inhibition, particularly of smooth  
 CC muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes,  
 CC chondrocytes and platelets. Peptidomimetics that mimic the protease  
 CC cleavage site in tropoelastin derivatives are competitive inhibitors of  
 CC the protease, and are used for protecting against lung damage caused by  
 CC elastin, for inhibiting or controlling localized growth of cancers or  
 CC metastases, or to limit protease activity that causes blood clotting

SQ Sequence 8 AA;

Alignment Scores:  
 Pred. NO.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAY69128 (1-8)

QY 3 TTGGCACTA 11

DB 5 LeuAlaLeu 7

RESULT 44

RAY84485

ID AAY84485 standard; peptide; 8 AA.

XX AC AAY84485;

XX 25-JUL-2000 (first entry)

XX DE Amino acid sequence of an epitopic fragment of the C-beta protein.  
 XX KW C-beta protein; bactericidal; gram positive bacteria; vaccine;  
 XX KW immune response.  
 XX OS Streptococcus agalactiae.  
 XX PN WO200015760-A1.  
 XX PD 23-MAR-2000.  
 XX PF 17-SEP-1999; 99WO-US021643.  
 XX PR 17-SEP-1998; 98US-0100859P.  
 XX PR 19-JUL-1999; 99US-0144324P.  
 XX PR 15-SEP-1999; 99US-0154017P.  
 XX PA (NAVA-) NORTH AMERICAN VACCINE INC.  
 XX PI Long-Rowe KO, Blake MS;  
 XX XX WPI; 2000-271404/23.  
 XX PT Obtaining substantially pure C-beta protein or fragment and/or mutant for  
 XX PT eliciting antibodies which are bactericidal to gram positive bacteria,  
 XX PT useful in vaccines.  
 XX PS Claim 19; Page 69; 171pp; English.  
 XX CC The specification describes a process for obtaining a substantially pure  
 XX CC C-beta protein. The process comprises obtaining the C-beta protein in  
 XX CC cell extracts, subjecting the C-beta protein to ion-exchange  
 XX CC chromatography and collecting the C-beta protein-containing fractions,  
 XX CC pooling and diluting the fractions, and subjecting the fractions to  
 XX CC ligand affinity chromatography and collection. The C-beta protein  
 XX CC fragments are useful for eliciting antibodies which are bactericidal to  
 XX CC gram positive bacteria with complement alone and therefore is useful in a  
 XX CC (combination) vaccine together with a pharmaceutically acceptable carrier  
 XX CC (and/or optionally at least two protein fragments or peptide-  
 XX CC polysaccharide conjugates). The vaccine therefore is useful in a method  
 XX CC for inducing an immune response in a mammal. The present sequence  
 XX CC represents an epitopic fragment derived from amino acids 827-1028 of the  
 XX CC Streptococcus agalactiae C-beta protein  
 XX SQ Sequence 8 AA;  
 Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-070-588A-112 (1-11) x AAY84485 (1-8)  
 Qy 9 GTGCCAAG 1  
 Db 1 ValProlys 3  
 RESULT 45  
 AAY84484  
 ID AAY84484 standard; peptide; 8 AA.  
 XX AC AAY84484;  
 XX XX  
 DT 25-JUL-2000 (first entry)  
 XX DE Amino acid sequence of an epitopic fragment of the C-beta protein.  
 XX KW C-beta protein; bactericidal; gram positive bacteria; vaccine;  
 XX KW immune response.

XX OS Streptococcus agalactiae.  
 XX PN WO200015760-A1.  
 XX PD 23-MAR-2000.  
 XX PF 17-SEP-1999; 99WO-US021643.  
 XX PR 17-SEP-1998; 98US-0100859P.  
 XX PR 19-JUL-1999; 99US-0144324P.  
 XX PR 15-SEP-1999; 99US-0154017P.  
 XX PA (NAVA-) NORTH AMERICAN VACCINE INC.  
 XX PI Long-Rowe KO, Blake MS;  
 XX XX WPI; 2000-271404/23.  
 XX PT Obtaining substantially pure C-beta protein or fragment and/or mutant for  
 XX PT eliciting antibodies which are bactericidal to gram positive bacteria,  
 XX PT useful in vaccines.  
 XX PS Claim 19; Page 69; 171pp; English.  
 XX CC The specification describes a process for obtaining a substantially pure  
 XX CC C-beta protein. The process comprises obtaining the C-beta protein in  
 XX CC cell extracts, subjecting the C-beta protein to ion-exchange  
 XX CC chromatography and collecting the C-beta protein-containing fractions,  
 XX CC pooling and diluting the fractions, and subjecting the fractions to  
 XX CC ligand affinity chromatography and collection. The C-beta protein  
 XX CC fragments are useful for eliciting antibodies which are bactericidal to  
 XX CC gram positive bacteria with complement alone and therefore is useful in a  
 XX CC (combination) vaccine together with a pharmaceutically acceptable carrier  
 XX CC (and/or optionally at least two protein fragments or peptide-  
 XX CC polysaccharide conjugates). The vaccine therefore is useful in a method  
 XX CC for inducing an immune response in a mammal. The present sequence  
 XX CC represents an epitopic fragment derived from amino acids 827-1028 of the  
 XX CC Streptococcus agalactiae C-beta protein  
 XX SQ Sequence 8 AA;  
 Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-070-588A-112 (1-11) x AAY84484 (1-8)  
 Qy 9 GTGCCAAG 1  
 Db 5 ValProlys 7  
 RESULT 46  
 AAY84483  
 ID AAY84483 standard; peptide; 8 AA.  
 XX AC AAY84483;  
 XX XX  
 DT 25-JUL-2000 (first entry)  
 XX DE Amino acid sequence of an epitopic fragment of the C-beta protein.  
 XX KW C-beta protein; bactericidal; gram positive bacteria; vaccine;  
 XX KW immune response.  
 XX OS Streptococcus agalactiae.  
 XX PN WO200015760-A1.  
 XX XX

```

PD 23-MAR-2000.
XX PF 17-SEP-1999; 99WO-US021643.
XX PR 17-SEP-1998; 98US-0100859P.
PR 19-JUL-1999; 99US-0144324P.
PR 15-SEP-1999; 99US-0154017P.
XX (NAVA-) NORTH AMERICAN VACCINE INC.
XX PA Long-Rowe KO, Blake MS;
XX PI WPI; 2000-271404/23.
XX DR
XX PT Obtaining substantially pure C-beta protein or fragment and/or mutant for
XX PT eliciting antibodies which are bactericidal to gram positive bacteria,
XX PT useful in vaccines.
XX PS Example 19; Page 69; 171pp; English.
XX CC The specification describes a process for obtaining a substantially pure
XX CC C-beta protein. The process comprises obtaining the C-beta protein in
XX CC cell extracts, subjecting the C-beta protein to ion-exchange
XX CC chromatography and collecting the C-beta protein-containing fractions,
XX CC pooling and diluting the fractions, and subjecting the fractions to
XX CC ligand affinity chromatography and collection. The C-beta protein
XX CC fragments are useful for eliciting antibodies which are bactericidal to
XX CC gram positive bacteria with complement alone and therefore is useful in a
XX CC (combination) vaccine together with a pharmaceutically acceptable carrier
XX CC (and/or optionally at least two protein fragments or peptide-
XX CC polysaccharide conjugates). The vaccine therefore is useful in a method
XX CC for inducing an immune response in a mammal. The present sequence
XX CC represents an epitopic fragment derived from amino acids 827-1028 of the
XX CC Streptococcus agalactiae C-beta protein
XX SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAY84483 (1-8)

QY 9 GTGCCAAG 1
DB 3 ValProLys 5

RESULT 47
AAY84500
ID AAY84500 standard; peptide; 8 AA.
AC AAY84500;
XX 25-JUL-2000 (first entry)
DT Amino acid sequence of a peptide derived from the C-beta protein.
DE C-beta protein; bactericidal; gram positive bacteria; vaccine;
XX immune response.
XX Streptococcus agalactiae.
XX WO200015760-A1.
XX 23-MAR-2000.
XX PF 17-SEP-1999; 99WO-US021643.
XX PR 17-SEP-1998; 98US-0100859P.
XX PR 19-JUL-1999; 99US-0144324P.
XX PR 15-SEP-1999; 99US-0154017P.
XX PA (NAVA-) NORTH AMERICAN VACCINE INC.
XX XX

PD 23-MAR-2000.
XX PF 17-SEP-1999; 99WO-US021643.
XX PR 17-SEP-1998; 98US-0100859P.
PR 19-JUL-1999; 99US-0144324P.
PR 15-SEP-1999; 99US-0154017P.
XX (NAVA-) NORTH AMERICAN VACCINE INC.
XX PA Long-Rowe KO, Blake MS;
XX PI WPI; 2000-271404/23.
XX DR
XX PT Obtaining substantially pure C-beta protein or fragment and/or mutant for
XX PT eliciting antibodies which are bactericidal to gram positive bacteria,
XX PT useful in vaccines.
XX PS Claim 19; Page 69; 171pp; English.
XX CC The specification describes a process for obtaining a substantially pure
XX CC C-beta protein. The process comprises obtaining the C-beta protein in
XX CC cell extracts, subjecting the C-beta protein to ion-exchange
XX CC chromatography and collecting the C-beta protein-containing fractions,
XX CC pooling and diluting the fractions, and subjecting the fractions to
XX CC ligand affinity chromatography and collection. The C-beta protein
XX CC fragments are useful for eliciting antibodies which are bactericidal to
XX CC gram positive bacteria with complement alone and therefore is useful in a
XX CC (combination) vaccine together with a pharmaceutically acceptable carrier
XX CC (and/or optionally at least two protein fragments or peptide-
XX CC polysaccharide conjugates). The vaccine therefore is useful in a method
XX CC for inducing an immune response in a mammal. The present sequence
XX CC represents an epitopic fragment derived from amino acids 827-1028 of the
XX CC Streptococcus agalactiae C-beta protein
XX SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAY84483 (1-8)

QY 9 GTGCCAAG 1
DB 3 ValProLys 5

RESULT 48
AAY84489
ID AAY84489 standard; peptide; 8 AA.
AC AAY84489;
XX 25-JUL-2000 (first entry)
DT Amino acid sequence of an epitopic fragment of the C-beta protein.
DE C-beta protein; bactericidal; gram positive bacteria; vaccine;
XX immune response.
XX Streptococcus agalactiae.
XX WO200015760-A1.
XX 23-MAR-2000.
XX PF 17-SEP-1999; 99WO-US021643.
XX PR 17-SEP-1998; 98US-0100859P.
XX PR 19-JUL-1999; 99US-0144324P.
XX PR 15-SEP-1999; 99US-0154017P.
XX PA (NAVA-) NORTH AMERICAN VACCINE INC.
XX XX

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PI Long-Rowe KO, Blake MS;  
 XX WPI; 2000-271404/23.  
 DR  
 XX  
 XX Obtaining substantially pure C-beta protein or fragment and/or mutant for  
 PT eliciting antibodies which are bactericidal to gram positive bacteria,  
 PT useful in vaccines.  
 XX  
 XX  
 PS Claim 19; Page 69; 171pp; English.  
 XX  
 XX The specification describes a process for obtaining a substantially pure  
 CC C-beta protein. The process comprises obtaining the C-beta protein in  
 CC cell extracts, subjecting the C-beta protein to ion-exchange  
 CC chromatography and collecting the C-beta protein-containing fractions,  
 CC pooling and diluting the fractions, and subjecting the fractions to  
 CC ligand affinity chromatography and collection. The C-beta protein  
 CC fragments are useful for eliciting antibodies which are bactericidal to  
 CC gram positive bacteria with complement alone and therefore is useful in a  
 CC (combination) vaccine together with a pharmaceutically acceptable carrier  
 CC (and/or optionally at least two protein fragments or peptide-  
 CC polysaccharide conjugates). The vaccine therefore is useful in a method  
 CC for inducing an immune response in a mammal. The present sequence  
 CC represents an epitopic fragment derived from amino acids 827-1028 of the  
 CC Streptococcus agalactiae C-beta protein  
 XX  
 SQ Sequence 8 AA;  
 Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-070-588A-112 (1-11) x AAY84489 (1-8)  
 Qy 3 TTGGCACTA 11  
 Db 5 LeuAlaLeu 7  
 RESULT 49  
 AAY69217  
 ID AAY69217 standard; peptide; 8 AA.  
 AC AAY69217;  
 XX  
 XX 30-MAY-2000 (first entry)  
 DT  
 XX  
 DE Tryptic peptide of honey bee venom PX3.101 protein.  
 XX  
 XX Protein PX3.101; honey bee; venom; interleukin-8; IL-8; receptor; CXCR1;  
 KW CXCR2; cyclooxygenase; lipoxigenase; phospholipase; protease;  
 KW inflammatory disease; gene therapy; cancer; autoimmune disease; pain;  
 KW chemokine imbalance; rheumatoid arthritis; multiple sclerosis; psoriasis;  
 KW systemic lupus erythematosus; Crohn's disease; vasculitis; scleroderma;  
 KW metastatic cancer; Alzheimer's disease; wound healing; aging process;  
 KW antigen.  
 XX  
 XX Apis mellifera.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1  
 FT /note= "unknown amino acid"  
 FT Misc-difference 2  
 FT /note= "unknown amino acid"  
 FT  
 XX GB2341389-A.  
 XX  
 XX 15-MAR-2000.  
 PD  
 XX  
 PF 13-SEP-1999; 99GB-00021605.  
 XX

PR 14-SEP-1998; 98US-0100172P.  
 XX (PANP-) PAN PACIFIC PHARM INC.  
 PA  
 XX  
 PI Chi X, Lu Y;  
 XX  
 DR WPI; 2000-185368/17.  
 XX  
 XX Isolated nucleic acids encoding the bee venom protein PX3.101 useful for  
 PT treating autoimmune and inflammatory disorders such as rheumatoid  
 PT arthritis.  
 PT  
 XX Example 2; Page 52; 83pp; English.  
 PS  
 XX The present sequence is derived from the protein PX3.101, which is a  
 CC honey bee venom isolated Apis mellifera. PX3.101 inhibits the binding of  
 CC interleukin-8 (IL-8) to its receptor (e.g. CXCR1 and CXCR2) and inhibits  
 CC a variety of enzymes (e.g. cyclooxygenases, lipoxigenases, phospholipases  
 CC and proteases) associated with inflammatory diseases. The nucleic acids  
 CC may be used for the recombinant production of PX3.101 proteins either in  
 CC vivo (as part of a gene therapy protocol) or in vitro (as a fermentation  
 CC culture). The nucleic acids may also be used as probes to identify  
 CC similar sequences in samples. The PX3.101 protein may be used for the  
 CC treatment of inflammatory diseases, cancers, autoimmune diseases, pain  
 CC and/or diseases associated with chemokine (especially IL-8) imbalances  
 CC such as rheumatoid arthritis, multiple sclerosis, psoriasis, systemic  
 CC lupus erythematosus (SLE), Crohn's disease, vasculitis, scleroderma,  
 CC metastatic cancer and Alzheimer's disease in humans. It is also disclosed  
 CC that the proteins may be used to accelerate wound healing, reduce several  
 CC aging processes and protect against ultraviolet light. The proteins may  
 CC also be used as antigens in the production of antibodies specific for  
 CC PX3.101. The antibodies may be used as diagnostic agents to detect  
 CC PX3.101 protein in samples and to down regulate PX3.101 activity  
 XX  
 SQ Sequence 8 AA;  
 Alignment Scores:  
 Pred. No.: 9.59e+07 Length: 8  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-070-588A-112 (1-11) x AAY69217 (1-8)  
 Qy 9 GTGCCAAG 1  
 Db 6 ValProllys 8  
 RESULT 50  
 AAB29524  
 ID AAB29524 standard; peptide; 8 AA.  
 XX  
 AC AAB29524;  
 XX  
 XX 14-FEB-2001 (first entry)  
 DT  
 XX  
 DE E9K peptide used in a Grb2 protein:peptide binding assay.  
 XX  
 KW Fluorescent dye; pH insensitive; trimethine cyanine analogue;  
 KW immunofluorescence detection system; fluorescence lifetime;  
 KW fluorescence polarisation; equilibrium-binding assay; binding-pair assay;  
 KW fluorescence resonance energy transfer; polarisation binding assay;  
 KW Grb2 protein; E9K peptide.  
 XX  
 OS Synthetic.  
 XX  
 XX US6133445-A.  
 PN  
 XX 17-OCT-2000.  
 PD  
 XX  
 PF 16-DEC-1998; 98US-00212564.  
 XX

XX 16-DEC-1998; 98US-00212564.  
XX (UYCA-) UNIV CARNEGIE MELLON.  
XX Waggoner AS, Mujumdar RB;  
XX WPI; 2000-678694/66.  
XX New bisindolinium(3,2-a,3',2'-a)pyrano(3,2-c;5,6-c')dipyridin-5-ium dye  
PT used as fluorescent marker and in fluorescence energy transfer complexes.  
PT Example 12; Col 27; 27pp; English.  
XX  
XX The invention relates to a novel analogue of a trimethine cyanine dye,  
CC 6,7,9,10-tetrahydro-2-carboxymethyl-14-sulphonato-16,16,18,18-  
CC tetramethyl-7aH,8aH-bisindolinium(3,2-a,3',2'-a)pyrano(3,2-c;5,6-  
CC c')dipyridin-5-ium. This compound can be used as a fluorescent marker and  
CC in fluorescence energy transfer complexes. It is a bright, highly  
CC fluorescent dye compound that absorbs and emits in the 450-600 nm region  
CC of the spectrum. It confers high quantum yields of fluorescence, is pH  
CC insensitive and extends the range of useful fluorescent labelling agents  
CC that can be used in fluorescent detection applications. The compound of  
CC the invention can be used in methods to determine the concentration of  
CC proteins or other components in a system, for example, in methods to  
CC measure the concentration of various labelled analytes using microtitre  
CC plate readers or other immunofluorescence detection systems. The novel  
CC dye may be used in assay methodologies that use fluorescent labels for  
CC the detection of analytes e.g., fluorescence resonance energy transfer  
CC (FRET)-based methods, fluorescence lifetime or fluorescence polarisation  
CC methods. It may be used in equilibrium-binding assays (e.g.,  
CC immunoassays, nucleic acid-hybridisation assays, protein-binding assays,  
CC hormone receptor assays), enzyme assays, proteolytic cleavage assays, and  
CC in nucleic acid or lipid cleavage assays). It may also be used in  
CC specific binding pair assays involving antibodies/antigens, lectins/  
CC glycoproteins, biotin/streptavidin, hormones/receptors, enzyme/  
CC substrate or co-factor, DNA/DNA, DNA/RNA or DNA/binding protein. The  
CC present sequence the E9K peptide which is specifically bound by the Grb2  
CC protein and which was used in a protein:peptide polarisation binding  
CC assay in an exemplification of the invention  
XX  
XX SQ Sequence 8 AA;

Alignment Scores:  
Pred. No.: 9.59e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAB29524 (1-8)

Qy 9 GTGCCAAG 1  
Db 6 ValProLys 8

Search completed: March 12, 2005, 11:05:46  
Job time : 66.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus n2p model

Run on: March 12, 2005, 10:58:23 ; Search time 15.5 Seconds  
(without alignments)  
136.566 Million cell upd

**Title:** US-10-070-588A-112

Perfect score: 3

Sequence: 1 ctttggccta 11

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Ygapop	60.0	Ygapext 60.0
Fgapop	60.0	Fgapext 7.0
Delop	6.0	Delext 7.0

Searched: 283416 seqs. 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565869

Minimum DB seq length: 0

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

**Command line parameters:**

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-DB=PR2.79 -USFPTO fastan -SUFFIX=oln2p.tpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=50 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HRAPIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FCAPEXT=7 -XGAPOP=60 -YGAPEXT=60 -DELEAF=7

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**Database :**

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	3	100.0	8	2	S37141	rpsA protein - Erw
C 2	3	100.0	9	2	S13333	alpha/beta-gliadin
C 3	3	100.0	11	2	S78765	ribosomal protein
C 4	3	100.0	11	2	S65377	cytochrome-c oxid
C 5	3	100.0	12	2	A26093	microbial collagen
C 6	3	100.0	12	2	A55837	5-aminimidazole r
C 7	3	100.0	12	2	PA0098	ribosomal protein
C 8	3	100.0	12	2	S07206	kassinin - Senegal
C 9	3	100.0	13	2	S31063	Ig lambda chain J
C 10	3	100.0	14	2	PA0094	hyocyanine (6s)-di
C 11	3	100.0	14	2	B34135	DNA-binding protei
C 12	3	100.0	14	2	PH0800	T-cell receptor al
C 13	3	100.0	14	2	PT0210	T-cell receptor al
C 14	3	100.0	14	2	S33801	chaperone, TCP1-re

88	3	100.0	25	2	S47204	T-cell receptor J-	161	3	100.0	30	2	B84786	hypothetical prote
89	3	100.0	25	2	S47211	T-cell receptor J-	162	3	100.0	30	2	B70165	hypothetical prote
90	3	100.0	25	2	S26651	uterglobin precu	163	3	100.0	30	2	A70209	hypothetical prote
91	3	100.0	25	2	PT0088	aryldialkylphospha	c 164	3	100.0	31	2	S13205	glyceraldehyde-3-p
92	3	100.0	25	2	B49111	POU homeodomain pr	c 165	3	100.0	31	2	S44472	Glucagon G2 - Nort
93	3	100.0	25	2	PH1907	T-cell receptor al	166	3	100.0	31	2	F53480	T-cell receptor al
94	3	100.0	25	2	S47190	T-cell receptor J-	167	3	100.0	31	2	T08489	hypothetical prote
95	3	100.0	25	2	I40061	shikimate 5-dehydr	168	3	100.0	31	2	F72429	hypothetical prote
96	3	100.0	25	2	T01689	ATPase-beta chain	c 169	3	100.0	31	2	C71845	hypothetical prote
97	3	100.0	25	2	I49409	CD2 antigen - west	170	3	100.0	31	2	C82175	hypothetical prote
98	3	100.0	25	2	S56002	glucan 1,3-beta-gl	171	3	100.0	31	2	B82466	hypothetical prote
99	3	100.0	25	2	S65729	hemoglobin, extrac	172	3	100.0	31	2	S15837	hypothetical prote
100	3	100.0	26	2	T12323	NADH2 dehydrogenas	173	3	100.0	31	2	T06934	photosystem I chai
101	3	100.0	26	2	T12327	NADH2 dehydrogenas	174	3	100.0	31	2	A05051	hypothetical prote
102	3	100.0	26	2	T13974	NADH2 dehydrogenas	175	3	100.0	31	2	S05124	hypothetical prote
103	3	100.0	26	2	T14217	NADH2 dehydrogenas	c 176	3	100.0	31	2	A36221	cecropin P1 - pig
104	3	100.0	26	2	T14221	NADH2 dehydrogenas	177	3	100.0	31	2	D82827	hypothetical prote
105	3	100.0	26	2	T14052	NADH2 dehydrogenas	178	3	100.0	31	2	T07290	photosystem I prot
106	3	100.0	26	2	S58384	NADH2 dehydrogenas	179	3	100.0	31	2	AD2046	hypothetical prote
107	3	100.0	26	2	A32806	T-cell receptor al	c 180	3	100.0	31	2	AD2046	hypothetical prote
108	3	100.0	26	2	F49164	transposase - Ech	181	3	100.0	32	2	PC2175	3alpha-hydroxyster
109	3	100.0	27	2	T12314	chromogranin-B - r	182	3	100.0	32	2	G46376	1-aminocyclopropan
110	3	100.0	27	2	T17064	NADH2 dehydrogenas	183	3	100.0	32	2	A53480	T-cell receptor al
111	3	100.0	27	2	T14017	NADH2 dehydrogenas	184	3	100.0	32	2	A02687	DNA-binding protei
112	3	100.0	27	2	T13836	NADH2 dehydrogenas	c 185	3	100.0	32	2	S11610	ribosomal protein
113	3	100.0	27	2	T17052	NADH2 dehydrogenas	186	3	100.0	32	2	PC7067	meltrin beta - mou
114	3	100.0	27	2	T17061	NADH2 dehydrogenas	187	3	100.0	32	2	E82279	hypothetical prote
115	3	100.0	27	2	T17055	NADH2 dehydrogenas	188	3	100.0	32	2	C82467	hypothetical prote
116	3	100.0	27	2	T17058	NADH2 dehydrogenas	189	3	100.0	32	2	H82416	hypothetical prote
117	3	100.0	27	2	T17067	NADH2 dehydrogenas	190	3	100.0	32	2	A05015	hypothetical prote
118	3	100.0	27	2	T12306	NADH2 dehydrogenas	191	3	100.0	32	2	C26393	callectrin - marb
119	3	100.0	27	2	T12310	NADH2 dehydrogenas	192	3	100.0	32	2	A36154	benzphetamine N-de
120	3	100.0	27	2	T12319	NADH2 dehydrogenas	193	3	100.0	33	2	S43312	2',3'-cyclic-nucle
121	3	100.0	27	2	T17070	NADH2 dehydrogenas	194	3	100.0	33	2	A44181	Cerastes serine pr
122	3	100.0	27	2	I46566	antileukoproteinas	c 195	3	100.0	33	2	A61310	nonhistone chromos
123	3	100.0	27	2	B60630	45k antigen - tric	c 196	3	100.0	33	2	I61694	myosin - human (fr
124	3	100.0	27	2	J50676	hypothetical 3.1k	197	3	100.0	33	2	T08018	ycf12 protein - Ch
125	3	100.0	27	2	G10002	transformation-sen	198	3	100.0	33	2	A05010	hypothetical prote
126	3	100.0	27	2	A12968	superoxide dismuta	199	3	100.0	33	2	E45557	orf immediately up
127	3	100.0	27	2	PC4234	hypothetical prote	200	3	100.0	33	2	B95133	neurofibromin - hu
128	3	100.0	27	2	H48200	homeotic protein H	c 201	3	100.0	33	2	E43675	hypothetical prote
129	3	100.0	27	2	B47295	homeodomain protei	202	3	100.0	33	2	A70159	hypothetical prote
130	3	100.0	28	2	T12301	NADH2 dehydrogenas	203	3	100.0	33	2	G82254	hypothetical prote
131	3	100.0	28	2	I46921	gene Bota protein	204	3	100.0	33	2	E82391	hypothetical prote
132	3	100.0	28	2	T14905	hypothetical prote	205	3	100.0	33	2	T03346	gene e21 protein -
133	3	100.0	28	2	S15235	hypothetical prote	206	3	100.0	33	2	E82553	hypothetical prote
134	3	100.0	28	2	S29285	arylalkyl acylamid	207	3	100.0	33	2	S18161	osteogenic protein
135	3	100.0	28	2	S63502	95k protein - Euba	c 208	3	100.0	34	2	A36626	class II histocomp
136	3	100.0	28	2	T06925	hypothetical prote	209	3	100.0	34	2	A19197	NADH2 dehydrogenas
137	3	100.0	29	1	Q1BP57	gene 1.5 protein -	c 210	3	100.0	34	2	S78345	hypothetical prote
138	3	100.0	29	2	C61233	conceptus protein	211	3	100.0	34	2	F84079	hypothetical prote
139	3	100.0	29	2	C47719	T-cell receptor al	212	3	100.0	34	2	E82819	hypothetical prote
140	3	100.0	29	2	I37306	HLA-DR beta - huma	213	3	100.0	34	2	HWGHD	hypothetical prote
141	3	100.0	29	2	I37534	Gene HLA-DRB prote	214	3	100.0	35	1	A05112	exendin-2 - Gilla m
142	3	100.0	29	2	I37536	MHC class II histo	c 215	3	100.0	35	2	S65772	M24 protein - Stre
143	3	100.0	29	2	I37303	HLA-DR beta - huma	216	3	100.0	35	2	S33666	hypothetical prote
144	3	100.0	29	2	I37535	gene HLA-DRB prote	217	3	100.0	35	2	B41161	23k antigen PEB2 -
145	3	100.0	29	2	PC4231	ribosomal protein	218	3	100.0	35	2	A45791	hypothetical prote
146	3	100.0	29	2	S26229	ribosomal protein	c 219	3	100.0	35	2	B69217	hypothetical prote
147	3	100.0	29	2	A35121	hypothetical prote	c 220	3	100.0	35	2	A39830	dentin matrix, inc
148	3	100.0	29	2	S05224	photosystem I 4.8K	c 221	3	100.0	35	2	A81346	hypothetical prote
149	3	100.0	29	2	G64674	hypothetical prote	222	3	100.0	35	2	S15821	venitricular natriu
150	3	100.0	29	2	G83440	KdGF protein PA163	c 223	3	100.0	36	2	S70806	hypothetical prote
151	3	100.0	29	2	T36654	probable small mem	224	3	100.0	36	2	S78721	protein YGL006w-a
152	3	100.0	29	2	S78326	conserved hypochet	225	3	100.0	36	2	A41017	T-cell receptor al
153	3	100.0	30	2	I57689	ubiquinol-cytochro	226	3	100.0	36	2	B53480	hypothetical prote
154	3	100.0	30	2	A05315	pancreatic ribonuc	227	3	100.0	36	2	D87544	hypothetical prote
155	3	100.0	30	2	A43937	endo-1,4-beta-xyla	228	3	100.0	36	2	A81740	hypothetical prote
156	3	100.0	30	2	D57001	endo-1,4-beta-xyla	229	3	100.0	36	2	E82854	hypothetical prote
157	3	100.0	30	2	PX0073	epoxide hydrolase	230	3	100.0	36	2	AH0066	hypothetical prote
158	3	100.0	30	2	B61511	serum albumin, mil	231	3	100.0	36	2	AB0592	probable membrane
159	3	100.0	30	2	S14355	4-sulfolbenzoate 3,	232	3	100.0	37	2	G95010	hypothetical prote
160	3	100.0	30	2	B46958	androgen-binding p	c 233	3	100.0	37	2		

234	3	100.0	37	2	G84233	hypothetical prote	c 307	3	100.0	42	2	A59483	alkaline phosphata
c 235	3	100.0	37	2	S41509	probable antimutat	c 308	3	100.0	42	2	H90761	hypothetical prote
236	3	100.0	37	2	B36511	hypothetical prote	c 309	3	100.0	42	2	E61399	hypothetical early
237	3	100.0	37	2	S03432	hypothetical prote	c 310	3	100.0	42	2	T46861	citrate synthase [
238	3	100.0	37	2	I49615	gamma-D-crystallin	c 311	3	100.0	42	2	F82691	hypothetical prote
239	3	100.0	37	2	C83780	hypothetical prote	c 312	3	100.0	42	2	T07077	heat shock protein
240	3	100.0	37	2	A81552	hypothetical prote	c 313	3	100.0	42	4	S36250	hypothetical prote
241	3	100.0	37	2	D82636	hypothetical prote	c 314	3	100.0	43	2	B41711	defensin B - beetl
242	3	100.0	37	2	S97596	hypothetical prote	c 315	3	100.0	43	2	C41711	defensin C - beetl
243	3	100.0	38	1	HWGHS	exendin-1 - Mexica	c 316	3	100.0	43	2	S48626	translati on elonga
244	3	100.0	38	2	I64844	SP-A1 (gamma, delt	c 317	3	100.0	43	2	T33020	hypothetical prote
c 245	3	100.0	38	2	T06938	photosystem II pro	c 318	3	100.0	43	2	T07224	hypothetical prote
c 246	3	100.0	38	2	S65416	pyruvate synthase	c 319	3	100.0	43	2	D95080	hypothetical prote
247	3	100.0	38	2	B82225	hypothetical prote	c 320	3	100.0	43	2	S31020	gene 75 protein -
c 248	3	100.0	38	2	F82495	hypothetical prote	c 321	3	100.0	43	2	E82428	hypothetical prote
249	3	100.0	38	2	B82413	hypothetical prote	c 322	3	100.0	43	2	D61219	serpin Spi 4 - hor
250	3	100.0	39	1	C59677	phosphatase (RapF)	c 323	3	100.0	43	2	H89887	hypothetical prote
251	3	100.0	39	2	S54330	trypsin inhibitor	c 324	3	100.0	43	2	E97379	hypothetical prote
252	3	100.0	39	2	I49418	insulin I precursor	c 325	3	100.0	44	2	FN0137	pepsin (EC 3.4.23.
253	3	100.0	39	2	S68791	ribosomal protein	c 326	3	100.0	44	2	FN0134	pepsin (EC 3.4.23.
254	3	100.0	39	2	S10315	photosystem II pro	c 327	3	100.0	44	2	D35878	class I major hist
255	3	100.0	39	2	S22880	gonadal protein gd	c 328	3	100.0	44	2	S00179	acidic ribosomal p
c 256	3	100.0	39	2	S67938	hypothetical prote	c 329	3	100.0	44	2	A61600	segmentation prote
c 257	3	100.0	39	2	C22102	phycoerythrin-545	c 330	3	100.0	44	2	A60731	photosystem II oxy
258	3	100.0	39	2	H95135	hypothetical prote	c 331	3	100.0	44	2	S54144	tnai protein - mou
259	3	100.0	39	2	S73118	photosystem II pro	c 332	3	100.0	44	2	AD0992	hypothetical prote
260	3	100.0	39	2	I37556	homeobox - human (	c 333	3	100.0	44	2	B84374	hypothetical prote
261	3	100.0	39	2	C81904	hypothetical prote	c 334	3	100.0	44	2	G64536	hypothetical prote
c 262	3	100.0	39	2	G82619	hypothetical prote	c 335	3	100.0	44	2	S39411	nosD protein - Par
263	3	100.0	39	2	C85911	hypothetical prote	c 336	3	100.0	44	2	D81921	hypothetical prote
264	3	100.0	39	2	A83109	hypothetical prote	c 337	3	100.0	44	2	D82364	hypothetical prote
265	3	100.0	40	2	A49081	capillary permeabi	c 338	3	100.0	44	2	E82225	hypothetical prote
266	3	100.0	40	2	S07969	T-cell receptor al	c 339	3	100.0	44	2	F97562	hypothetical prote
267	3	100.0	40	2	S43028	ribosomal protein	c 340	3	100.0	44	4	IMBP8	hypothetical immun
c 268	3	100.0	40	2	I64846	SP-2A gamma - huma	c 341	3	100.0	44	4	IMBP10	hypothetical immun
c 269	3	100.0	40	2	S5907	conglutin gamma -	c 342	3	100.0	45	1	F2YB2K	photosystem II pro
c 270	3	100.0	40	2	A59494	alkaline phosphata	c 343	3	100.0	45	2	H44530	T-cell receptor al
c 271	3	100.0	40	2	S95169	hypothetical prote	c 344	3	100.0	45	2	S10051	ribosomal protein
c 272	3	100.0	40	2	F90439	hypothetical prote	c 345	3	100.0	45	2	E64508	hypothetical prote
273	3	100.0	40	2	A64530	hypothetical prote	c 346	3	100.0	45	2	T26203	hypothetical prote
274	3	100.0	40	2	D83378	hypothetical prote	c 347	3	100.0	45	2	C85625	hypothetical prote
c 275	3	100.0	40	2	G82507	hypothetical prote	c 348	3	100.0	45	2	E85762	hypothetical prote
c 276	3	100.0	40	2	T11811	hypothetical prote	c 349	3	100.0	45	2	D97513	hypothetical prote
277	3	100.0	40	2	I45887	elastin - bovine (	c 350	3	100.0	46	1	ACBP4	gene ac protein -
278	3	100.0	40	2	F81511	hypothetical prote	c 351	3	100.0	46	2	I37047	NADH2 dehydrogenas
279	3	100.0	41	2	I49419	insulin II precurs	c 352	3	100.0	46	2	S45724	peptidylprolyl iso
c 280	3	100.0	41	2	S26936	Ig heavy chain V r	c 353	3	100.0	46	2	S29490	GRF-binding protei
c 281	3	100.0	41	2	S45008	ribosomal protein	c 354	3	100.0	46	2	S23288	light-harvesting p
c 282	3	100.0	41	2	E82556	50S ribosomal prot	c 355	3	100.0	46	2	S11162	photosystem II pro
c 283	3	100.0	41	2	D82269	probable ribosomal	c 356	3	100.0	46	2	A41814	somatotropin recep
c 284	3	100.0	41	2	I64840	SP-A2 delta - huma	c 357	3	100.0	46	2	T28799	hypothetical prote
c 285	3	100.0	41	2	S07673	light-harvesting p	c 358	3	100.0	46	2	C83437	hypothetical prote
c 286	3	100.0	41	2	A50620	probable bacteriop	c 359	3	100.0	46	2	S10024	lipopeptide uppl p
c 287	3	100.0	41	2	S38918	hypothetical prote	c 360	3	100.0	46	2	FQ0040	agrD protein - Sta
c 288	3	100.0	41	2	B70240	hypothetical prote	c 361	3	100.0	46	2	S61282	nikkomycin synthet
c 289	3	100.0	41	2	D82458	hypothetical prote	c 362	3	100.0	46	2	G89761	hypothetical prote
c 290	3	100.0	41	2	H82422	hypothetical prote	c 363	3	100.0	46	2	B97522	hypothetical prote
c 291	3	100.0	41	2	T35359	hypothetical prote	c 364	3	100.0	47	2	E46376	1-aminocyclopropan
c 292	3	100.0	41	2	C82793	hypothetical prote	c 365	3	100.0	47	2	AC0380	probable ribosomal
c 293	3	100.0	41	2	G82657	hypothetical prote	c 366	3	100.0	47	2	B46544	major iron-regulat
c 294	3	100.0	41	2	F82525	hypothetical prote	c 367	3	100.0	47	2	S23289	light-harvesting p
c 295	3	100.0	41	2	C97327	hypothetical prote	c 368	3	100.0	47	2	S03396	probable regulator
c 296	3	100.0	41	4	I68622	hypothetical mveli	c 369	3	100.0	47	2	D87675	hypothetical prote
c 297	3	100.0	42	1	WNBP1	gene i protein - p	c 370	3	100.0	47	2	A82254	hypothetical prote
c 298	3	100.0	42	2	A34259	cytochrome P450mt4	c 371	3	100.0	47	2	F69284	ISORF2 homolog ISA
c 299	3	100.0	42	2	D85650	hypothetical prote	c 372	3	100.0	47	2	A81730	hypothetical prote
c 300	3	100.0	42	2	T07294	photosystem II pro	c 373	3	100.0	47	2	D81666	hypothetical prote
c 301	3	100.0	42	2	S00692	probable photosyst	c 374	3	100.0	48	1	RSVF32	ribosomal protein
c 302	3	100.0	42	2	G56271	lrfA 5'-region hyp	c 375	3	100.0	48	2	S68885	light-harvesting p
c 303	3	100.0	42	2	A53312	purine-nucleoside	c 376	3	100.0	48	2	S68886	light-harvesting p
c 304	3	100.0	42	2	T36992	probable transposa	c 377	3	100.0	48	2	S15246	fimb protein - Dic
c 305	3	100.0	42	2	D22102	phycoerythrin-545	c 378	3	100.0	48	2	B86452	protein F6N18.9 [i
c 306	3	100.0	42	2	T07324	hypothetical prote	c 379	3	100.0	48	2	B64647	hypothetical prote

380	3	100.0	48	2	D83223	hypothetical prote	453	3	100.0	52	2	G82699	hypothetical prote
381	3	100.0	48	2	D81237	hypothetical prote	454	3	100.0	52	2	G89939	hypothetical prote
382	3	100.0	48	2	D69402	hypothetical prote	455	3	100.0	52	4	T11818	hypothetical Pdlec
383	3	100.0	48	2	S10588	cysteine proteinas	456	3	100.0	53	2	S60540	H+-transporting tw
384	3	100.0	48	2	T13337	hypothetical prote	c 457	3	100.0	53	2	T11962	ribosomal protein
385	3	100.0	48	2	F81452	50S ribosomal prot	458	3	100.0	53	2	I64235	ribosomal protein
386	3	100.0	49	2	G44530	T-cell receptor al	459	3	100.0	53	2	S73696	ribosomal protein
387	3	100.0	49	2	S27047	N-formylmethanofur	460	3	100.0	53	2	E64365	hypothetical prote
388	3	100.0	49	2	S58145	hypothetical prote	461	3	100.0	53	2	T27982	hypothetical prote
389	3	100.0	49	2	F90528	hypothetical prote	462	3	100.0	53	2	S17672	hypothetical prote
390	3	100.0	49	2	H87397	hypothetical prote	c 463	3	100.0	53	2	B87570	hypothetical prote
391	3	100.0	49	2	H81233	conserved hypothet	464	3	100.0	53	2	B87671	hypothetical prote
392	3	100.0	49	2	H82006	hypothetical prote	465	3	100.0	53	2	B81079	hypothetical prote
393	3	100.0	49	2	H75292	hypothetical prote	466	3	100.0	53	2	F69358	hypothetical prote
394	3	100.0	49	2	J01600	rapC' protein - Cl	467	3	100.0	53	2	J50105	hypothetical prote
395	3	100.0	49	2	S66219	defensin AMP1 - Cl	468	3	100.0	53	2	S77336	exoskeletal protei
396	3	100.0	49	2	G84034	hypothetical prote	469	3	100.0	53	2	A56512	nuclear pore prote
397	3	100.0	49	2	C71316	hypothetical prote	470	3	100.0	53	2	D83832	hypothetical prote
398	3	100.0	49	2	AG3362	hypothetical prote	c 471	3	100.0	53	2	G82546	hypothetical prote
399	3	100.0	49	2	I48681	185 kDa glycophosp	472	3	100.0	53	2	A95335	hypothetical prote
400	3	100.0	50	2	T06541	probable NADPH-fer	473	3	100.0	53	2	G95302	hypothetical prote
401	3	100.0	50	2	I53729	metalloproteinase	474	3	100.0	53	2	F89871	hypothetical prote
402	3	100.0	50	2	I80356	MHC HLA-DR-beta ch	475	3	100.0	53	2	AF1734	hypothetical prote
403	3	100.0	50	2	S14125	hypothetical prote	c 476	3	100.0	53	2	C98129	hypothetical prote
404	3	100.0	50	2	FQ0547	capsid protein VP2	477	3	100.0	53	2	AG2338	hypothetical prote
405	3	100.0	50	2	S40969	TyB protein - yeas	c 478	3	100.0	54	1	QCBP3L	regulatory protein
406	3	100.0	50	2	S77603	ccoH protein - Par	c 479	3	100.0	54	2	S78292	ribosomal protein
407	3	100.0	50	2	D65040	small protein A -	c 480	3	100.0	54	2	S34541	hypothetical prote
408	3	100.0	50	2	C85908	small membrane pro	c 481	3	100.0	54	2	E91003	regulatory protein
409	3	100.0	50	2	G91063	small membrane pro	c 482	3	100.0	54	2	B99776	regulatory protein
410	3	100.0	50	2	AG3298	hypothetical prote	483	3	100.0	54	2	S45255	YjJX protein homol
411	3	100.0	50	2	C34643	cathepsin E (EC 3.	484	3	100.0	54	2	T07284	hypothetical prote
412	3	100.0	50	2	C72257	hypothetical prote	c 485	3	100.0	54	2	AC0896	conserved hypochet
413	3	100.0	50	2	B82279	hypothetical prote	c 486	3	100.0	54	2	AF0729	hypothetical prote
c 414	3	100.0	50	2	S32546	cytochrome c555 -	c 487	3	100.0	54	2	AF0729	hypothetical prote
c 415	3	100.0	50	2	T08019	hypothetical prote	c 488	3	100.0	54	2	F81886	hypothetical prote
416	3	100.0	50	2	T29687	hypothetical prote	c 489	3	100.0	54	2	F81135	hypothetical prote
417	3	100.0	50	2	A81540	hypothetical prote	c 490	3	100.0	54	2	H82450	hypothetical prote
418	3	100.0	50	2	C82773	hypothetical prote	491	3	100.0	54	2	G69733	phage-related prot
419	3	100.0	50	2	G82652	hypothetical prote	492	3	100.0	54	2	D69949	chad protein [impo
420	3	100.0	50	2	H82588	hypothetical prote	493	3	100.0	54	2	T44940	hypothetical prote
421	3	100.0	50	2	G85912	hypothetical prote	494	3	100.0	54	2	T45629	hypothetical prote
422	3	100.0	50	2	S78674	hypothetical prote	c 495	3	100.0	54	2	C82836	hypothetical prote
423	3	100.0	50	4	I55615	hypothetical ORF n	c 496	3	100.0	54	2	C82603	hypothetical prote
424	3	100.0	51	1	B32541	histatin 3 precurs	497	3	100.0	54	2	H82596	hypothetical prote
c 425	3	100.0	51	2	I36691	cytochrome-C3 hydr	c 498	3	100.0	54	2	A99918	hypothetical prote
c 426	3	100.0	51	2	A56371	collagen alpha 1(X	499	3	100.0	54	2	AB2291	hypothetical prote
427	3	100.0	51	2	G90818	hypothetical prote	c 500	3	100.0	54	2	AB2291	hypothetical prote
428	3	100.0	51	2	F90912	hypothetical prote							
429	3	100.0	51	2	A98164	probable ATP-depen							
430	3	100.0	51	2	B90140	hypothetical prote							
431	3	100.0	51	2	B45246	orf 3' of ldh - lac							
432	3	100.0	51	2	T36214	spcC protein - Str							
433	3	100.0	51	2	T30077	hypothetical prote							
c 434	3	100.0	51	2	E82833	hypothetical prote							
c 435	3	100.0	51	2	F82759	hypothetical prote							
436	3	100.0	51	2	G85730	hypothetical prote							
437	3	100.0	51	2	E89778	hypothetical prote							
438	3	100.0	51	2	AE3604	protein ybgt [impo							
439	3	100.0	51	2	D81271	small hydrophobic							
c 440	3	100.0	51	2	AH1840	hypothetical prote							
c 441	3	100.0	52	2	F44530	T-cell receptor al							
c 442	3	100.0	52	2	S37208	ribosomal protein							
443	3	100.0	52	2	S13501	major oleosin rad-							
c 444	3	100.0	52	2	S60854	M protein precurs							
445	3	100.0	52	2	T13197	hypothetical prote							
446	3	100.0	52	2	AG0730	hypothetical prote							
447	3	100.0	52	2	E96798	hypothetical prote							
448	3	100.0	52	2	JQ1261	hypothetical prote							
449	3	100.0	52	2	G69527	hypothetical 5.8K							
c 450	3	100.0	52	2	G69527	ISA1214-6, ISORF2							
c 451	3	100.0	52	2	A69330	ISORF2-like protei							
452	3	100.0	52	2	S63981	immune-inducible p							

## ALIGNMENTS

## RESULT 1

S37141

rpsA protein - Erwinia chrysanthemi

C;Species: Erwinia chrysanthemi

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C;Accession: S37141

R;Douillie, A.; Toussaint, A.; Faelen, M.

submitted to the EMBL Data Library, August 1993

A;Description: Identification of the integration host factor genes of E. chrysanthemi.

A;Reference number: S37139

A;Accession: S37141

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-8 &lt;DOU&gt;

A;Cross-references: UNIPROT:P37985; EMBL:X74750; NID:g399669; PIDN:CAA52769.1; PID:g5811

Alignment Scores:

Pred. No.: 2.41e+07

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Length: 8

Matches: 3

Conservative: 0

Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S37141 (1-8)

Qy 10 AGTGCCAAA 2  
Db 4 SerAlaLeu 6

RESULT 2  
alpha/beta-gliadin - wheat (fragment)  
C/Species: Triticum aestivum (common wheat)  
C/Date: 19-Mar-1997 #sequence\_revision 30-Jan-1998 #text\_change 09-Jul-2004  
C/Accession: S13333  
R/Arvan, A.P.; An, G.; Okita, T.W.  
Mol. Gen. Genet. 225, 65-71, 1991  
A/Title: Structural and functional analysis of promoter from gliadin, an endosperm-specific protein  
A/Reference number: S13333; MUID:91155936; PMID:2000092  
A/Accession: S13333  
A/Molecule type: DNA  
A/Residues: 1-9 <ARY>  
A/Cross-references: UNIPROT:Q41531; UNIPROT:Q41529; UNIPROT:Q41546; UNIPROT:Q41530; UNIPROT:Q41537

Alignment Scores:  
Pred. No.: 2.14e+07 Length: 9  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S13333 (1-9)

Qy 3 TTGGCACTA 11  
Db 7 LeuAlaLeu 9

RESULT 3  
S78765  
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: S78765  
R/Graack, H.R.  
submitted to the Protein Sequence Database, July 1999  
A/Reference number: S78760  
A/Accession: S78765  
A/Molecule type: protein  
A/Residues: 1-11 <GRA>  
A/Cross-references: UNIPROT:Q7M374  
C/Keywords: mitochondrion  
F/1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Alignment Scores:  
Pred. No.: 8.91e+04 Length: 11  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S78765 (1-11)

Qy 9 GTGCCAAG 1  
Db 5 ValProLys 7

RESULT 4  
S65377  
cytochrome-c oxidase (EC 1.9.3.1) chain Via-H, cardiac - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S65377  
R/Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A/Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
A/Reference number: S65372; MUID:95324529; PMID:7601105  
A/Accession: S65377  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <SCH>  
A/Cross-references: UNIPROT:Q7MOD4  
C/Keywords: cardiac muscle; heart; oxidoreductase

Alignment Scores:  
Pred. No.: 8.91e+04 Length: 11  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S65377 (1-11)

Qy 10 AGTGCCAAA 2  
Db 2 SerAlaLys 4

RESULT 5  
A26093  
microbial collagenase (EC 3.4.24.3) 1 - Vibrio alginolyticus chemovar. iophagus (fragment)  
N/Alternate names: Achromobacter collagenase  
C/Species: Vibrio alginolyticus chemovar. iophagus  
C/Date: 24-Jun-1987 #sequence\_revision 02-Jun-1988 #text\_change 03-May-1994  
C/Accession: A26093  
R/Tong, N.T.; Teugita, A.; Keil-DiLouha, V.  
Biochim. Biophys. Acta 874, 295-304, 1986  
A/Reference number: A26093  
A/Accession: A26093  
A/Molecule type: protein  
A/Residues: 1-12 <TON>  
C/Keywords: hydrolase; metalloproteinase

Alignment Scores:  
Pred. No.: 8.65e+04 Length: 12  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A26093 (1-12)

Qy 3 TTGGCACTA 11  
Db 9 LeuAlaLeu 11

RESULT 6  
A55837  
5-aminoimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminoimidazole  
C/Species: Gallus gallus (chicken)  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 17-Mar-1999  
C/Accession: A55837  
R/Firestine, S.M.; Davisson, V.J.  
Biochemistry 33, 11917-11926, 1994  
A/Title: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gal  
A/Reference number: A55837; MUID:95001903; PMID:7918410  
A/Accession: A55837  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <FIR>

Alignment Scores:  
Pred. No.: 8.65e+04 Length: 12  
Score: 3.00 Matches: 3

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 2

US-10-070-588A-112 (1-11) x A55837 (1-12)  
QY 3 TTGGCACTA 11  
DB 6 LeuAlaLeu 8

## RESULT 7

PA0098  
ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)  
C/Species: Fusarium sporotrichioides  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
R/Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Taugita, A.  
submitted to JIPID, October 1994  
A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
A/Reference number: PA0051  
A/Accession: PA0098  
A/Molecule type: protein  
A/Residues: 1-12 <CHO>  
A/Cross-references: UNIPROT:Q7M4X9

Alignment Scores:  
Pred. No.: 8.65e+04 Length: 12  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 2

US-10-070-588A-112 (1-11) x PA0098 (1-12)

QY 9 GTGCCAAAG 1  
DB 6 ValProllys 8

## RESULT 8

S07206  
kassinin - Senegal running frog  
C/Species: Kassina senegalensis (Senegal running frog)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 16-Aug-2004  
C/Accession: S07206  
R/Anastasi, A.; Montecucchi, P.; Erspamer, V.; Visser, J.  
Experientia 33, 857-858, 1977  
A/Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide from Senegal  
A/Reference number: S07206; MUID:77246385; PMID:891753  
A/Accession: S07206  
A/Molecule type: protein  
A/Residues: 1-12 <ANA>  
A/Cross-references: UNIPROT:P08611  
C/Keywords: amidated carboxyl end  
P/12/Modified site: amidated carboxyl end (Met) #status experimental

Alignment Scores:  
Pred. No.: 8.65e+04 Length: 12  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 2

US-10-070-588A-112 (1-11) x S07206 (1-12)

QY 9 GTGCCAAAG 1  
DB 2 ValProllys 4

## RESULT 9

S03063

Ig lambda chain J region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 11-Jan-2002  
C/Accession: S03063

R/Udey, J.A.; Blomberg, B.B.  
Nucleic Acids Res. 16, 2959-2969, 1988  
A/Title: Intergenic exchange maintains identity between two human lambda light chain immunoglobulin genes  
A/Reference number: S03063; MUID:88217512; PMID:3130611  
A/Accession: S03063  
A/Molecule type: DNA  
A/Residues: 1-13 <UDE>  
A/Cross-references: EMBL:X06877; NID:g33357; PIDN:CAA29996.1; PID:g1335162  
C/Keywords: heterotetramer; immunoglobulin

Alignment Scores:  
Pred. No.: 8.42e+04 Length: 13  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 2

US-10-070-588A-112 (1-11) x S03063 (1-13)

QY 2 TTGGCACT 10  
DB 3 PheGlyThr 5

## RESULT 10

PA0094  
hyocyanine (6s)-dioxygenase II - fungus (Fusarium sporotrichioides) (fragment)  
C/Species: Fusarium sporotrichioides  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C/Accession: PA0094  
R/Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Taugita, A.  
submitted to JIPID, October 1994  
A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
A/Reference number: PA0051  
A/Accession: PA0094  
A/Molecule type: protein  
A/Residues: 1-14 <CHO>

Alignment Scores:  
Pred. No.: 8.21e+04 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 2

US-10-070-588A-112 (1-11) x PA0094 (1-14)

QY 3 TTGGCACTA 11  
DB 11 LeuAlaLeu 13

## RESULT 11

B34135  
DNA-binding protein q - Crithidia fasciculata mitochondrion (fragment)  
C/Species: mitochondrion Crithidia fasciculata  
C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 07-Dec-1999  
C/Accession: B34135  
R/Tittawella, I.  
FEBS Lett. 260, 57-61, 1990  
A/Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata  
A/Reference number: A34135  
A/Accession: B34135  
A/Molecule type: protein  
A/Residues: 1-14 <TIT>  
C/Genetics:  
A/Genome: mitochondrion  
A/Genetic code: SGC6  
C/Keywords: mitochondrion

Alignment Scores:  
Pred. No.: 8.21e+04 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x B34135 (1-14)

Qy 10 AGTGCCAAA 2

Db 5 SerAlalys 7

RESULT 12

PH0800  
T-cell receptor alpha chain (J3) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PH0800  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0800

A;Molecule type: mRNA

A;Residues: 1-14 <CAS>

A;Cross-references: EMBL:X60907

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 8.21e+04 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PH0800 (1-14)

Qy 10 AGTGCCAAA 2

Db 8 SerAlalys 10

RESULT 13

PT0210

T-cell receptor alpha chain V-J region (4-1-K.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C;Accession: PT0210  
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0210

A;Molecule type: mRNA

A;Residues: 1-14 <NAK>

C;Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 8.21e+04 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PT0210 (1-14)

Qy 10 AGTGCCAAA 2

Db 12 SerAlalys 14

RESULT 14

S33801

Chaperone, TCP1-related - oat

C;Species: Avena sativa (oat)

C;Date: 02-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: S33801

R;Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Schaefer

Nature 363, 644-648, 1993

A;Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its photo

A;Reference number: S33800; MUID:93288140; PMID:8099715

A;Accession: S33801

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <MUM>

A;Cross-references: UNIPROT:Q7M1G7

Alignment Scores:

Pred. No.: 8.21e+04 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S33801 (1-14)

Qy 10 AGTGCCAAA 2

Db 4 SerAlalys 6

RESULT 15

S33802

Chaperone, TCP1-related - oat

C;Species: Avena sativa (oat)

C;Date: 02-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: S33802

R;Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Schaefer

Nature 363, 644-648, 1993

A;Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its photo

A;Reference number: S33800; MUID:93288140; PMID:8099715

A;Accession: S33802

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <MUM>

A;Cross-references: UNIPROT:Q7M1G6

Alignment Scores:

Pred. No.: 8.21e+04 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S33802 (1-14)

Qy 10 AGTGCCAAA 2

Db 4 SerAlalys 6

RESULT 16

PA0076

fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (Fusarium sporotrichioides) (frag

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C;Accession: PA0076

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A;Reference number: PA0051

A;Accession: PA0076  
A;Molecule type: protein  
A;Residues: 1-15 <CHO>  
C;Keywords: aldehyde-lyase; carbon-carbon lyase

Alignment Scores:  
Pred. No.: 8.02e+04 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PA0076 (1-15)

Qy 10 AGTGCCAAA 2  
Db 1 SerAlalys 3

## RESULT 17

14K protein - California sea hare (fragment)  
C;Species: Aplysia californica (California sea hare)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Feb-1994  
C;Accession: D60977  
R;Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.  
Electrophoresis 10, 152-157, 1989  
A;Title: Development of a database of amino acid sequences for proteins identified and  
A;Reference number: A60977; MUID:89276264; PMID:2731514  
A;Accession: D60977  
A;Molecule type: protein  
A;Residues: 1-15 <SWE>

Alignment Scores:  
Pred. No.: 8.02e+04 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x D60977 (1-15)

Qy 3 TTGGCACTA 11  
Db 2 LeuAlaleu 4

## RESULT 18

formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)  
C;Species: Alcaligenes eutrophus  
C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S59492  
R;Friedebold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.  
Biol. Chem. Hoppe-Seyler 376, 561-568, 1995  
A;Title: Structural and immunological studies on the soluble formate dehydrogenase from  
A;Reference number: S59492; MUID:96145736; PMID:8561915  
A;Accession: S59492  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <PRI>  
A;Cross-references: UNIPROT:O87815

Alignment Scores:  
Pred. No.: 8.02e+04 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S59492 (1-15)

Qy 2 TTGGCACT 10  
Db 9 PheGlyThr 11

## RESULT 19

CQRT  
cerebellin - rat  
N;Contains: des-Ser-cerebellin  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 09-Jul-2004  
C;Accession: A03135  
R;Slemmon, J.R.; Blacher, R.; Danho, W.; Hempstead, J.L.; Morgan, J.I.  
Proc. Natl. Acad. Sci. U.S.A. 81, 6866-6870, 1984  
A;Title: Isolation and sequencing of two cerebellum-specific peptides.  
A;Reference number: A03135  
A;Accession: A03135  
A;Molecule type: protein  
A;Residues: 1-16 <SLE>  
A;Cross-references: UNIPROT:P23436  
C;Comment: The sequence of des-Ser-cerebellin lacks 1-Ser.  
C;Comment: The cerebellin is localized in the Purkinje cells of rat cerebellum.  
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hom  
C;Keywords: brain

Alignment Scores:  
Pred. No.: 7.85e+04 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x CQRT (1-16)

Qy 10 AGTGCCAAA 2  
Db 3 SerAlalys 5

## RESULT 20

S66613  
protein p12E - Friend murine leukemia virus (fragments)  
C;Species: Friend murine leukemia virus  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S66613  
R;Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.  
Eur. J. Biochem. 232, 373-380, 1995  
A;Title: Localization of the palmitoylation site in the transmembrane protein p12E of Fr  
A;Reference number: S66613; MUID:96035869; PMID:7556184  
A;Accession: S66613  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9;10-16 <HEN>

Alignment Scores:  
Pred. No.: 7.85e+04 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S66613 (1-16)

Qy 3 TTGGCACTA 11  
Db 7 LeuAlaleu 9

## RESULT 21

B60566  
cytochrome P450m51a - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 05-May-1993  
C;Accession: B60566



R;Negata, K.; Martin, B.M.; Gillette, J.R.; Sasame, H.A.  
Drug Metab. Dispos. 18, 557-564, 1990  
A;Title: Isozymes of cytochrome P-450 that metabolize naphthalene in liver and lung of  
A;Reference number: A60566; MUID:91168724; PMID:1981702  
A;Accession: B60566  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <NAG>

Alignment Scores:  
Pred. No.: 7.85e+04 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x B60566 (1-16)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 7 LeuAlaLeu 9

## RESULT 22

PH1476  
T-cell receptor beta chain (clone 223/14) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 15-Mar-2004  
C;Accession: PH1476  
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko  
J. Exp. Med. 177, 811-820, 1993  
A;Title: T cell receptor selection by and recognition of two class I major histocompatib  
A;Reference number: PH1430; MUID:93171821; PMID:8436911  
A;Accession: PH1476  
A;Molecule type: mRNA  
A;Residues: 1-16 <CAS>  
A;Experimental source: cytolytic T-lymphocyte  
C;Keywords: receptor; T-cell

Alignment Scores:  
Pred. No.: 7.85e+04 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PH1476 (1-16)

Qy 2 TTGGCACT 10  
| | | | |  
Db 5 PheGlyThr 7

## RESULT 23

PH1474  
T-cell receptor beta chain (clone A2/25) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 15-Mar-2004  
C;Accession: PH1474  
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko  
J. Exp. Med. 177, 811-820, 1993  
A;Title: T cell receptor selection by and recognition of two class I major histocompatib  
A;Reference number: PH1430; MUID:93171821; PMID:8436911  
A;Accession: PH1474  
A;Molecule type: mRNA  
A;Residues: 1-16 <CAS>  
A;Experimental source: cytolytic T-lymphocyte  
C;Keywords: receptor; T-cell

Alignment Scores:  
Pred. No.: 7.85e+04 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PH1474 (1-16)

Qy 2 TTGGCACT 10  
| | | | |  
Db 5 PheGlyThr 7

## RESULT 24

S11760  
flgL protein - Caulobacter crescentus (fragment)  
C;Species: Caulobacter crescentus  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: PQ0126; A25882; S11760  
R;Schoenlein, P.V.; Gallman, L.S.; Winkler, M.E.; Ely, B.  
Gene 93, 17-25, 1990  
A;Title: Nucleotide sequence of the Caulobacter crescentus flaF and flbT genes and an an  
A;Reference number: JQ0741; MUID:91033011; PMID:1699845  
A;Accession: PQ0126  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-16 <SCH>  
A;Cross-references: UNIPROT:P18914; GB:X15134; NID:G40418; PIDN:CAA33232.1; PID:G40422  
R;Minnich, S.A.; Newton, A.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1142-1146, 1987  
A;Title: Promoter mapping and cell cycle regulation of flagellin gene transcription in C  
A;Reference number: A25882; MUID:87147229; PMID:3469658  
A;Accession: A25882  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-12, 'V', 14-16 <MIN>  
A;Cross-references: GB:M15688; NID:G144267; PIDN:AAA23050.1; PID:G144269  
C;Genetics:  
A;Gene: flgL

Alignment Scores:  
Pred. No.: 7.85e+04 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S11760 (1-16)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 13 LeuAlaLeu 15

## RESULT 25

A61268  
cytochrome P450-thc - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 05-Mar-1999  
C;Accession: A61268  
R;Bornheim, L.M.; Correia, M.A.  
Mol. Pharmacol. 40, 228-234, 1991  
A;Title: Purification and characterization of the major hepatic cannabinoid hydroxylase  
A;Reference number: A61268; MUID:91342605; PMID:1875910  
A;Accession: A61268  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <BOR>  
C;Genetics:  
A;Gene: Cyp2c29  
C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology  
C;Keywords: heme

Alignment Scores:  
Pred. No.: 7.85e+04 Length: 16  
Score: 3.00 Matches: 3

Percent Similarity: 100.00%    Conservative: 0  
Best Local Similarity: 100.00%    Mismatches: 0  
Query Match: 100.00%    Indels: 0  
DB: 2    Gaps: 0

US-10-070-588A-112 (1-11) x A61268 (1-16)

Qy 3 TTGGCACTA 11

Db 7 LeuAlaLeu 9

RESULT 26

PL0124

cerebellin - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 16-Aug-2004

C/Accession: PL0124

R/Yianguo, Y.; Burnet, P.; Nikou, G.; Chrysanthou, B.J.; Bloom, S.R.

J. Neurochem. 53, 886-889, 1989

A/Title: Purification and characterisation of cerebellins from human and porcine cerebell

A/Reference number: PL0124; MUID:89341798; PMID:2760624

A/Accession: PL0124

A/Molecule type: protein

A/Residues: 1-16 <YIA>

A/Cross-references: UNIPROT:P23435; UNIPROT:P23436

A/Experimental source: brain

A/Note: the sequences of human and porcine cerebellin are identical to that of the rat

C/Comment: The peptide is identified in two molecular forms having 16 and 15 amino acid

Alignment Scores:

Pred. No.: 7.85e+04    Length: 16

Score: 3.00    Matches: 3

Percent Similarity: 100.00%    Conservative: 0

Best Local Similarity: 100.00%    Mismatches: 0

Query Match: 100.00%    Indels: 0

DB: 2    Gaps: 0

US-10-070-588A-112 (1-11) x PL0124 (1-16)

Qy 10 AGTGCCAAA 2

Db 3 SerAlaLys 5

RESULT 27

I51910

SP-A2 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C/Accession: I51910

R/McCormick, S.M.; Boggaram, V.; Mendelson, C.R.

Am. J. Physiol. 266, L354-L366, 1994

A/Title: Characterization of mRNA transcripts and organization of human SP-A1 and SP-A2

A/Reference number: I51910; MUID:94234365; PMID:8179012

A/Accession: I51910

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-17 <RES>

A/Cross-references: UNIPROT:P78490; GB:S69679; NID:G546669; PIDN:AAB30729.1; PID:G546670

C/Genetics:

A/Gene: SP-A2

C/Superfamily: mannose-binding lectin; C-type lectin homology

Alignment Scores:

Pred. No.: 7.69e+04    Length: 17

Score: 3.00    Matches: 3

Percent Similarity: 100.00%    Conservative: 0

Best Local Similarity: 100.00%    Mismatches: 0

Query Match: 100.00%    Indels: 0

DB: 2    Gaps: 0

US-10-070-588A-112 (1-11) x I51910 (1-17)

Qy 3 TTGGCACTA 11

Db 6 LeuAlaLeu 8

RESULT 28

S47201

T-cell receptor J-alpha wntv.3 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 05-Nov-1999

C/Accession: S47201

R/Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.

submitted to the EMBL Data Library, February 1993

A/Reference number: S40133

A/Accession: S47201

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-17 <PIA>

A/Cross-references: EMBL:X71048; NID:G506944; PIDN:CAA50365.1; PID:G510661

C/Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 7.69e+04    Length: 17

Score: 3.00    Matches: 3

Percent Similarity: 100.00%    Conservative: 0

Best Local Similarity: 100.00%    Mismatches: 0

Query Match: 100.00%    Indels: 0

DB: 2    Gaps: 0

US-10-070-588A-112 (1-11) x S47201 (1-17)

Qy 2 TTGGCACT 10

Db 7 PheGlyThr 9

RESULT 29

PH0778

T-cell receptor alpha chain (RA10.3.3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C/Accession: PH0778

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilesky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-r

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; MUID:92078846; PMID:1836010

A/Accession: PH0778

A/Molecule type: mRNA

A/Residues: 1-17 <CAS>

A/Cross-references: EMBL:X60875

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 7.69e+04    Length: 17

Score: 3.00    Matches: 3

Percent Similarity: 100.00%    Conservative: 0

Best Local Similarity: 100.00%    Mismatches: 0

Query Match: 100.00%    Indels: 0

DB: 2    Gaps: 0

US-10-070-588A-112 (1-11) x PH0778 (1-17)

Qy 10 AGTGCCAAA 2

Db 11 SerAlaLys 13

RESULT 30

C56211

progesterone receptor-related protein p23 - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 20-Jun-2000

C/Accession: C56211

R/Johnson, J.L.; Beito, T.G.; Krco, C.J.; Toft, D.O.

Mol. Cell. Biol. 14, 1956-1963, 1994

A>Title: Characterization of a novel 23-kilodalton protein of unactive progesterone receptor  
A/Reference number: A56211; MUID:94158868; PMID:9114727  
A/Accession: C56211  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-18 <OH>  
C/Superfamily: Caenorhabditis elegans hypothetical protein ZC395.10  
C/Keywords: steroid hormone receptor

Alignment Scores:  
Pred. No.: 7.54e+04 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x C56211 (1-18)

Qy 10 AGTGCCAAA 2  
Db 5 SerAlaLys 7

RESULT 31  
140062  
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
C/Species: Buchnera aphidicola  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999  
C/Accession: I40062  
R/Roubaksh, D.; Baumann, P.  
Gene 155, 107-112, 1995  
A/Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endosymbiont)  
A/Reference number: I40061; MUID:95212914; PMID:7535281  
A/Accession: I40062  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-18 <RES>  
A/Cross-references: EMBL:U10496; NID:9854711; PIDN:AAA79125.1; PID:9854712  
C/Genetics:  
A/Gene: aroB  
C/Keywords: oxidoreductase

Alignment Scores:  
Pred. No.: 7.54e+04 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I40062 (1-18)

Qy 1 CTTGGGCAC 9  
Db 4 LeuTrpHis 6

RESULT 32  
S78767  
ribosomal protein MRP-S29, mitochondrial - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C/Accession: S78767  
R/Graack, H.R.  
submitted to the Protein Sequence Database, July 1999  
A/Reference number: S78760  
A/Accession: S78767  
A/Molecule type: protein  
A/Residues: 1-18 <GRA>  
C/Keywords: mitochondrion  
F/1-18/Product: ribosomal protein MRP-S29 (fragment) #status experimental <MAT>

Alignment Scores:  
Pred. No.: 7.54e+04 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S78767 (1-18)

Qy 3 TTGGCACTA 11  
Db 3 LeuAlaLeu 5

RESULT 33  
159649  
human leukocyte antigen alpha chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: I59649  
R/Fogdell, A.; Olerup, O.  
Tissue Antigens 44, 19-24, 1994  
A/Title: The DOA1\*0104 allele is carried by DRB1\*1001- and DRB1\*1401-positive haplotypes  
A/Reference number: I59649; MUID:95064785; PMID:7974465  
A/Accession: I59649  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-18 <RES>  
A/Cross-references: UNIPROT:Q30216; GB:S75685; NID:g913771; PIDN:AAB32621.1; PID:g913772  
C/Genetics:  
A/Gene: GDB:H1A-DOA1  
A/Cross-references: GDB:I20638; OMIM:146880  
A/Map position: 6p21.3-6p21.3

Alignment Scores:  
Pred. No.: 7.54e+04 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I59649 (1-18)

Qy 3 TTGGCACTA 11  
Db 3 LeuAlaLeu 5

RESULT 34  
S70611  
30K protein - Engelmannia pinnatifida (fragment)  
C/Species: Engelmannia pinnatifida  
C/Date: 14-Apr-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C/Accession: S70611  
R/Huynh, Q.K.; Borgmeyer, J.R.; Smith, C.E.; Bell, L.D.; Shah, D.M.  
Biochem. J. 316, 723-727, 1996  
A/Title: Isolation and characterization of a 30 kDa protein with antifungal activity from  
A/Reference number: S70611; MUID:96265034; PMID:8670144  
A/Accession: S70611  
A/Molecule type: protein  
A/Residues: 1-18 <HUY>  
A/Cross-references: UNIPROT:Q10722  
A/Experimental source: leaves  
C/Keywords: antifungal

Alignment Scores:  
Pred. No.: 7.54e+04 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S70611 (1-18)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 10 LeuAlaLeu 12

RESULT 35  
I53673  
amyloid protein - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 13-Aug-1999  
C/Accession: I53673  
R/Chernak, J.M.  
Gene 133, 255-260, 1993  
A/Title: Structural features of the 5' upstream regulatory region of the gene encoding  
A/Reference number: I53673; MUID:94040820; PMID:8224912  
A/Accession: I53673  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-19 <RES>  
A/Cross-references: GB:L11926; NID:g949984; PIDN:AAA74458.1; PID:g202962  
C/Genetics:  
A/Gen: APP  
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Alignment Scores:  
Pred. No.: 7.41e+04 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I53673 (1-19)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 5 LeuAlaLeu 7

RESULT 36  
beta-1,3-glucan-binding protein - signal crayfish (fragment)  
C/Species: Pacifastacus leniusculus (signal crayfish)  
C/Date: 17-Aug-1990 #sequence\_revision 17-Aug-1990 #text\_change 18-Jun-1993  
C/Accession: A35301  
R/Duvic, B.; Soederhaell, K.  
J. Biol. Chem. 265, 9327-9332, 1990  
A/Title: Purification and characterization of a beta-1,3-glucan binding protein from pla  
A/Reference number: A35301; MUID:90264428; PMID:2111817  
A/Accession: A35301  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-19 <DUV>

Alignment Scores:  
Pred. No.: 7.41e+04 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A35301 (1-19)

Qy 10 AGTGCCAAA 2  
| | | | |  
Db 13 SerAlaLys 15

RESULT 37  
B46592  
lactase-phlorizin hydrolase 140K isoform - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 01-Nov-1996  
C/Accession: B46592  
R/Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutchens, T.W.; Nichols, B.L.; Rosenberger, J

J. Biol. Chem. 268, 13609-13616, 1993  
A/Title: In vivo sucrose-isomaltase and lactase-phlorizin hydrolase turnover in the fed  
A/Reference number: A46592; MUID:93293888; PMID:8514793  
A/Accession: B46592  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-19 <DUV>  
A/Note: sequence extracted from NCBI backbone (NCBIP:134560)  
C/Keywords: carbohydrate digestion; intestine

Alignment Scores:  
Pred. No.: 7.41e+04 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x B46592 (1-19)

Qy 9 GTGCCAAG 1  
| | | | |  
Db 9 ValProLys 11

RESULT 38  
A41077  
protein-disulfide reductase (glutathione) (BC 1.8.4.2) Q-5 - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 23-Jun-1993  
C/Accession: A41077  
R/Srivastava, S.P.; Chen, N.; Liu, Y.; Holtzman, J.L.  
J. Biol. Chem. 266, 20337-20344, 1991  
A/Title: Purification and characterization of a new isozyme of thiol:protein-disulfide o  
fic phospholipase C form 1A.  
A/Reference number: A41077; MUID:92041865; PMID:1657921  
A/Accession: A41077  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-19 <SRI>  
C/Keywords: oxidoreductase

Alignment Scores:  
Pred. No.: 7.41e+04 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A41077 (1-19)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 1 LeuAlaLeu 3

RESULT 39  
B60822  
cytochrome P450 UT50 - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-2004  
C/Accession: B60822  
R/Ameliazad, Z.; Narbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.  
Biochem. Pharmacol. 37, 3245-3249, 1988  
A/Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.  
A/Reference number: A60822; MUID:88293549; PMID:3041969  
A/Accession: B60822  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-19 <AME>  
A/Cross-references: UNIPROT:Q7M068  
C/Genetics:  
A/Gen: CYP2C  
C/Superfamily: cytochrome P450 homology

C;Keywords: heme

Alignment Scores:  
Pred. No.: 7.41e+04 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x B60822 (1-19)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 7 LeuAlaLeu 9

RESULT 40

S11471  
A;Title: 25-hydroxyvitamin D(3) 25-monoxygenase (EC 1.14.14.-) cytochrome P450D2, kidney - pig  
N;Alternate names: 25-hydroxyvitamin D(3) 25-hydroxylase; cytochrome P450(25)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 05-Mar-1999  
C;Accession: S11471  
R;Bergman, T.; Postlind, H.  
Biochem. J. 270, 345-350, 1990  
A;Title: Characterization of pig kidney microsomal cytochrome P-450 catalysing 25-hydrox  
A;Reference number: S11471; MUID:90380027; PMID:2169238  
A;Accession: S11471  
A;Molecule type: Protein  
A;Residues: 1-20 <BER>  
C;Genetics:  
A;Gene: CYP2D  
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C;Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S11471 (1-20)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 11 LeuAlaLeu 13

RESULT 41

A23739  
Cytochrome P450 MUT-2, hepatic - mouse (fragment)  
N;Contains: oxidoreductase (EC 1.-.-.-)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-Mar-1999  
C;Accession: A23739  
R;Watanabe, K.; Narimatsu, S.; Yamamoto, I.; Yoshimura, H.  
J. Biol. Chem. 266, 2709-2711, 1991  
A;Title: Oxygenation mechanism in conversion of aldehyde to carboxylic acid catalyzed by  
A;Reference number: A23739; MUID:91131554; PMID:1847130  
A;Accession: A23739  
A;Molecule type: Protein  
A;Residues: 1-20 <WAT>  
C;Genetics:  
A;Gene: Cyp2c  
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A23739 (1-20)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 7 LeuAlaLeu 9

RESULT 42

A60822  
Cytochrome P450 PB-3a - rat (fragment)  
N;Contains: oxidoreductase (EC 1.-.-.-)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: A60822; I55191  
R;Ameliazad, Z.; Narbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.  
Biochem. Pharmacol. 37, 3245-3249, 1988  
A;Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.  
A;Reference number: A60822; MUID:88293549; PMID:3041969  
A;Accession: A60822  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <AME>  
A;Cross-references: UNIPROT:P04167  
R;Hashimoto, T.; Matsumoto, T.; Nishizawa, M.; Kawabata, S.  
J. Biochem. 103, 487-492, 1988  
A;Title: A mutant rat strain deficient in induction of a phenobarbital-inducible form o  
A;Reference number: I55191; MUID:88273074; PMID:2839467  
A;Accession: I55191  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-20 <RES>  
A;Cross-references: GB:D00250; NID:Q220727; PIDN:BAA00181.1; PID:Q220728  
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protei

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A60822 (1-20)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 9 LeuAlaLeu 11

RESULT 43

S30381  
Glutathione transferase (EC 2.5.1.18) class mu chain 7.2 - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 02-Dec-1993 #sequence\_revision 08-Nov-1996 #text\_change 09-Jul-2004  
C;Accession: S30381  
R;Primiano, T.; Novak, R.F.  
Arch. Biochem. Biophys. 301, 404-410, 1993  
A;Title: Purification and characterization of class mu glutathione S-transferase isozyme  
A;Reference number: S30380; MUID:93213177; PMID:8460949  
A;Accession: S30381  
A;Molecule type: protein  
A;Residues: 1-20 <PRI>  
A;Cross-references: UNIPROT:Q9TQ08  
C;Superfamily: Glutathione transferase  
C;Keywords: dimer; transferase

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
US-10-070-588A-112 (1-11) x S30381 (1-20)  
Qy 3 TTGGCACTA 11  
Db 12 LeuAlaLeu 14  
RESULT 44  
A60489  
venombin A (EC 3.4.21.74) - cantil (fragment)  
N/Alternate names: Agkistrodon bilineatus serine proteinase; alpha-fibrinogenase; ancro  
C/Species: Agkistrodon bilineatus (Cantil)  
C/Date: 19-Mar-1993 #sequence\_revision 19-Mar-1993 #text\_change 09-Jul-2004  
C/Accession: A60489  
R/Nakagaki, T.; Kazim, A.L.; Kisiel, W.  
Thromb. Res. 58, 593-602, 1990  
A/Title: Isolation and characterization of a protein C activator from tropical moccasin  
A/Reference number: A60489; MUID:90350102; PMID:2385829  
A/Accession: A60489  
A/Molecule type: Protein  
A/Residues: 1-20 <NA>  
A/Cross-references: UNIPROT:P33588  
C/Superfamily: trypsin; trypsin homology  
C/Keywords: glycoprotein; hydrolase; serine proteinase; venom

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A60489 (1-20)

Qy 3 TTGGCACTA 11  
Db 15 LeuAlaLeu 17

RESULT 45  
PN0133  
pepsin (EC 3.4.23.-) 1 - horse (fragment)  
N/Alternate names: pepsin (pI 1.8)  
C/Species: Equus caballus (domestic horse)  
C/Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
C/Accession: PN0133  
R/Gonchar, M.V.; Lavrenova, G.I.; Rudenskaya, G.N.; Gaida, A.V.; Stepanov, V.M.  
Biochimia 49, 1026-1037, 1984  
A/Title: Multiple forms of horse pepsin.  
A/Reference number: PN0133; MUID:84281135; PMID:6432065  
A/Accession: PN0133  
A/Molecule type: protein  
A/Residues: 1-20 <GON>  
A/Cross-references: UNIPROT:Q7M3D6  
A/Note: article in Russian with English abstract  
C/Superfamily: pepsin  
C/Keywords: aspartic proteinase; hydrolase; protein digestion

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PN0133 (1-20)

Qy 2 TTGGCACT 10  
Db 15 PheGlyThr 17

## RESULT 46

PL0192  
Ig lambda 2 chain - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
C/Accession: PL0192  
R/Alonso, A.; Chang, L.A.; Murialdo, H.  
Mol. Immunol. 27, 115-127, 1990  
A/Title: Analysis of the expression of murine lambda genes transfected into immunocompet  
A/Reference number: PL0192; MUID:90205873; PMID:2108323  
A/Accession: PL0192  
A/Molecule type: DNA  
A/Residues: 1-20 <ALO>  
C/Genetics:  
A/Introns: 16/2  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PL0192 (1-20)

Qy 3 TTGGCACTA 11  
Db 11 LeuAlaLeu 13

## RESULT 47

I38417  
HLA-A11 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C/Accession: I38417  
R/Balas, A.; Garcia-Sanchez, F.; Gomez-Reino, F.; Vicario, J.L.  
Hum. Immunol. 41, 69-73, 1994  
A/Title: HLA class I allele (HLA-A2) expression defect associated with a mutation in its  
A/Reference number: I38417; MUID:95137784; PMID:7836067  
A/Accession: I38417  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-20 <RES>  
A/Cross-references: UNIPROT:O19618; EMBL:U02934; NID:9414543; PIDN:AAA76607.1; PID:94145

C/Superfamily: class I histocompatibility antigen; immunoglobulin homology

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I38417 (1-20)

Qy 3 TTGGCACTA 11  
Db 17 LeuAlaLeu 19

## RESULT 48

I38418  
HLA-A2 - human (fragment)  
N/Alternate names: HLA-A23  
C/Species: Homo sapiens (man)  
C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C/Accession: I38418; I38419  
R/Balas, A.; Garcia-Sanchez, F.; Gomez-Reino, F.; Vicario, J.L.  
Hum. Immunol. 41, 69-73, 1994

A:Title: HLA class I allele (HLA-A2) expression defect associated with a mutation in its  
A:Reference number: 138417; MUID:95137784; PMID:7836067  
A:Accession: 138418  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-20 <RES>  
A:Cross-references: UNIPROT:P01892; UNIPROT:O19620; EMBL:U02935; NID:g414545; PIDN:AAA76

A:Accession: 138419  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-20 <RE2>  
A:Cross-references: EMBL:U02936; NID:g414547; PIDN:AAA76609.1; PID:g414548  
C:Genetics:  
A:Gene: HLA-2; HLA-23  
A:Map position: 6p21.3  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I38418 (1-20)

Qy 3 TTGGCACTA 11  
| | | | |  
Db 17 LeuAlaLeu 19

#### RESULT 49

D49255  
T-cell receptor beta chain V-D-J-C region (V beta 12, J beta 2.4) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C:Accession: D49255  
R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.  
Eur. J. Immunol. 22, 541-549, 1992  
A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A:Reference number: A49039; MUID:92164737; PMID:1311263  
A:Accession: D49255  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-20 <ROS>  
A:Note: sequence extracted from NCBI backbone (NCBIP:90725)  
C:Keywords: T-cell receptor

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x D49255 (1-20)

Qy 10 AGTCCAAA 2  
| | | | |  
Db 12 SerAlaLys 14

#### RESULT 50

A54538  
39k major outer membrane protein - Actinobacillus actinomycetemcomitans (strain Y4) (fra  
C:Species: Actinobacillus actinomycetemcomitans  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: A54538  
R:Koikeguchi, S.; Kato, K.; Nishimura, P.; Kurihara, H.; Murayama, Y.  
FEMS Microbiol. Lett. 77, 85-90, 1991  
A:Title: Isolation and partial characterization of a 39 kDa major outer membrane protein  
A:Reference number: A54538  
A:Accession: A54538

A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <KOK>  
A:Cross-references: UNIPROT:P20242

Alignment Scores:  
Pred. No.: 7.28e+04 Length: 20  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A54538 (1-20)

Qy 2 TTGGCACT 10  
| | | | |  
Db 7 PheGlyThr 9

Search completed: March 12, 2005, 11:08:11  
Job time : 27.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 10:28:53 ; Search time 50.5 Seconds  
(without alignments)  
223.084 Million cell updates/sec

Title: US-10-070-588A-112

Perfect score: 3

Sequence: 1 cttgggacta ll

Scoring table: OLIGO 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3224203

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODE=frame+ n2p.model -DEV=xlh  
-Q/cn2\_1/USPTO spool/US10070588/runat\_10032005\_120705\_15240/app\_query.fasta\_1.199  
-DB=Uniprot\_03 -Qfmt=fastan -Suffix=olin2p.rup -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=500 -DOALIGN=200 -THR SCORE=quality -THR\_MIN=1 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10070588 @CGN 1 1 140 @runat\_10032005\_120705\_15240 -NCPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	3	100.0	8	1	RS1 ERWCH
C 2	3	100.0	8	2	Q6JC68
C 3	3	100.0	9	2	Q9MW43
C 4	3	100.0	10	1	Q9MW43
C 5	3	100.0	10	1	Q9MW43
C 6	3	100.0	10	2	Q50843
C 7	3	100.0	10	2	Q78225
C 8	3	100.0	10	2	Q9SM70
C 9	3	100.0	10	2	Q8SAC2
C 10	3	100.0	10	2	Q9S905
C 11	3	100.0	11	2	Q9C1R7
C 12	3	100.0	11	2	Q7M374
C 13	3	100.0	11	2	Q9UEX7
C 14	3	100.0	11	2	Q6QV9
C 15	3	100.0	11	2	Q7MOD4
C 16	3	100.0	12	1	TKN_KASSE

Q8J0A7	12	2	100.0	12	2	Q8J0A7	Q8J0A7	saccharomy
Q7M4X9	12	2	100.0	12	2	Q7M4X9	Q7M4X9	fusarium sp
Q96PH0	12	2	100.0	12	2	Q96PH0	Q96PH0	homo sapien
Q31851	12	2	100.0	12	2	Q31851	Q31851	arabidopsis
Q6J6C7	12	2	100.0	12	2	Q6J6C7	Q6J6C7	glycine max
Q9UE87	13	2	100.0	13	2	Q9UE87	Q9UE87	homo sapien
Q6SE60	13	2	100.0	13	2	Q6SE60	Q6SE60	drosophila
Q7RAS8	13	2	100.0	13	2	Q7RAS8	Q7RAS8	plasmodium
Q39380	13	2	100.0	13	2	Q39380	Q39380	brassicica ol
Q6URV3	13	2	100.0	13	2	Q6URV3	Q6URV3	sorghum bic
Q62352	13	2	100.0	13	2	Q62352	Q62352	mus musculu
Q62354	13	2	100.0	13	2	Q62354	Q62354	mus musculu
Q62355	13	2	100.0	13	2	Q62355	Q62355	mus musculu
Q9PWP4	13	2	100.0	13	2	Q9PWP4	Q9PWP4	discoetichu
1 FERT TOBAC	14	1	100.0	14	1	1 FERT TOBAC	1 FERT TOBAC	nicotiana t
1 UC34 MAIZE	14	1	100.0	14	1	1 UC34 MAIZE	1 UC34 MAIZE	zea mays (m
Q6J0V5	14	2	100.0	14	2	Q6J0V5	Q6J0V5	sus scrofa
Q9TRQ7	14	2	100.0	14	2	Q9TRQ7	Q9TRQ7	bos taurus
Q714T6	14	2	100.0	14	2	Q714T6	Q714T6	prymesium
Q9MRV1	14	2	100.0	14	2	Q9MRV1	Q9MRV1	allium vera (
Q9MRV4	14	2	100.0	14	2	Q9MRV4	Q9MRV4	allium sati
Q9MT61	14	2	100.0	14	2	Q9MT61	Q9MT61	allium porr
Q64224	14	2	100.0	14	2	Q64224	Q64224	allium cepa
Q64225	14	2	100.0	14	2	Q64225	Q64225	brachytheci
Q64228	14	2	100.0	14	2	Q64228	Q64228	brachytheci
Q643A0	14	2	100.0	14	2	Q643A0	Q643A0	brachytheci
Q7M1G6	14	2	100.0	14	2	Q7M1G6	Q7M1G6	avena sativ
Q7M1G7	14	2	100.0	14	2	Q7M1G7	Q7M1G7	avena sativ
Q9FUX5	14	2	100.0	14	2	Q9FUX5	Q9FUX5	symphoricar
Q8VU21	14	2	100.0	14	2	Q8VU21	Q8VU21	streptococc
Q711Z6	14	2	100.0	14	2	Q711Z6	Q711Z6	lactobacill
Q9UR64	15	2	100.0	15	2	Q9UR64	Q9UR64	pleurotus o
Q9MZRS	15	2	100.0	15	2	Q9MZRS	Q9MZRS	oryctolagus
Q9TQ55	15	2	100.0	15	2	Q9TQ55	Q9TQ55	mus sp. maj
Q6XBM6	15	2	100.0	15	2	Q6XBM6	Q6XBM6	platylomell
Q76MM2	15	2	100.0	15	2	Q76MM2	Q76MM2	eurypharyn
Q931E6	15	2	100.0	15	2	Q931E6	Q931E6	chloroflex
Q6QQR4	15	2	100.0	15	2	Q6QQR4	Q6QQR4	helicobacte
Q8F5G1	15	2	100.0	15	2	Q8F5G1	Q8F5G1	spermophilu
C 57	16	1	100.0	16	1	C 57	C 57	sus scrofa
C 58	16	1	100.0	16	1	C 58	C 58	rattus norv
C 59	16	1	100.0	16	1	C 59	C 59	solanan tub
C 60	16	1	100.0	16	1	C 60	C 60	methanobact
C 61	16	2	100.0	16	2	C 61	C 61	saccharomyc
C 62	16	2	100.0	16	2	C 62	C 62	homo sapien
C 63	16	2	100.0	16	2	C 63	C 63	plasmodium
C 64	16	2	100.0	16	2	C 64	C 64	bos taurus
C 65	16	2	100.0	16	2	C 65	C 65	fejevarya
C 66	16	2	100.0	16	2	C 66	C 66	platylomell
C 67	16	2	100.0	16	2	C 67	C 67	arabidopsis
C 68	16	2	100.0	16	2	C 68	C 68	pinus conto
C 69	16	2	100.0	16	2	C 69	C 69	treponema d
C 70	16	2	100.0	16	2	C 70	C 70	rattus sp.
C 71	16	2	100.0	16	2	C 71	C 71	gallus gall
C 72	16	2	100.0	16	2	C 72	C 72	gallus gall
C 73	17	2	100.0	17	2	C 73	C 73	neurospora
C 74	17	2	100.0	17	2	C 74	C 74	gallus gall
C 75	17	2	100.0	17	2	C 75	C 75	methanococc
C 76	17	2	100.0	17	2	C 76	C 76	homo sapien
C 77	17	2	100.0	17	2	C 77	C 77	homo sapien
C 78	17	2	100.0	17	2	C 78	C 78	homo sapien
C 79	17	2	100.0	17	2	C 79	C 79	platylomell
C 80	17	2	100.0	17	2	C 80	C 80	platylomell
C 81	17	2	100.0	17	2	C 81	C 81	streptococc
C 82	17	2	100.0	17	2	C 82	C 82	lactococcus
C 83	17	2	100.0	17	2	C 83	C 83	newcastle d
C 84	17	2	100.0	17	2	C 84	C 84	gallus gall
C 85	17	2	100.0	17	2	C 85	C 85	gallus gall
C 86	18	2	100.0	18	2	C 86	C 86	neurospora
C 87	18	2	100.0	18	2	C 87	C 87	oryctolagus
C 88	18	2	100.0	18	2	C 88	C 88	homo sapien
C 89	18	2	100.0	18	2	C 89	C 89	homo sapien
C 90	18	2	100.0	18	2	C 90	C 90	homo sapien
C 91	18	2	100.0	18	2	C 91	C 91	bacterioph
C 92	18	2	100.0	18	2	C 92	C 92	engelmannia
C 93	18	2	100.0	18	2	C 93	C 93	sorghum bic
C 94	18	2	100.0	18	2	C 94	C 94	eschericia
C 95	18	2	100.0	18	2	C 95	C 95	lactobacill
C 96	18	2	100.0	18	2	C 96	C 96	lactobacill

Q8J0A7	saccharomy
Q7M4X9	fusarium sp
Q96PH0	homo sapien
Q31851	arabidopsis
Q6J67	glycine max
Q9UE87	homo sapien
Q6SE60	drosophila
Q7RAS8	plasmodium
Q39380	brassica ol
Q6URV3	sorghum bic
Q62352	mus musculus
Q62354	mus musculus
Q62355	mus musculus
Q9PWP4	discothecha
P82150	nicotiana t
P80640	zea mays (m
Q6J0V5	sus scrofa
Q9TRQ7	bos taurus
Q714T6	prymnesium
Q9MRV1	aloe vera (
Q9MRV4	allium sati
Q9MT61	allium pori
Q64224	allium cepa
Q64225	brachytheci
Q64228	brachytheci
Q643A0	brachytheci
Q7M1G6	avena sativ
Q7M1G7	avena sativ
Q9FUX5	symphoricar
Q8VU21	streptococc
Q711Z6	lactobacill
Q9UR64	pleurotus o
Q9MZRS	oryctolegus
Q9TQ55	mus sp. maj
Q6XBM6	platylomell
Q76MM2	eurypharynx
Q931E6	chloroflexu
Q6QQR4	helicobacte
Q8F5G1	spermophilu
P63181	sus scrofa
P63182	rattus norv
P80501	solanan tub
Q9UWK4	methanobact
Q8J1R1	saccharomyc
Q6NSY3	homo sapien
Q7RJE1	plasmodium
Q6LCS7	bos taurus
P92732	fejevarya
Q6XBM8	platylomell
Q680Q0	arabidopsis
Q9S8H7	pinus conto
Q9R5S7	treponema d
Q9QV11	rattus sp.
Q9PSL6	gallus gall
Q50842	methanococc
P78490	homo sapien
Q96DJ6	homo sapien
Q6XBM7	platylomell
Q9S889	naresissus p
Q6LEF2	streptococc
Q8GJN9	lactobacill
Q98Y55	newcastlec d
Q90XE2	gallus gall
Q9S9C7	neurospora
Q8SQ45	oryctolegus
Q30216	homo sapien
Q9TNP1	mus sp. m
Q37852	bacterioph
Q10722	engelmannia
Q6URV5	sorghum bic
Q06514	escherichia
Q53503	lactobacill

90	3	100.0	18	2	Q9QW64	Q9qwg4 mus musculus	163	3	100.0	21	2	O25621	O25621 helicobacte
91	3	100.0	18	2	Q9WUQ6	Q9wug6 mus musculus	164	3	100.0	21	2	Q6RSN3	Q6rsn3 mus musculus
c 92	3	100.0	18	2	O13167	O13167 xiphias gla	165	3	100.0	21	2	Q9QUW4	Q9quw4 mus sp. a
93	3	100.0	19	1	TLB1_BONJA	P81882 bothrops ja	166	3	100.0	22	2	Q8NHD8	Q8nhd8 homo sapien
c 94	3	100.0	19	2	Q6PKG8	Q6pkg8 homo sapien	c 167	3	100.0	22	2	Q9UCE2	Q9uce2 homo sapien
95	3	100.0	19	2	Q9H2B3	Q9h2b3 homo sapien	168	3	100.0	22	2	Q9UN58	Q9un58 homo sapien
c 96	3	100.0	19	2	Q68M63	Q68m63 ciona intes	c 169	3	100.0	22	2	O44123	O44123 plasmodium
97	3	100.0	19	2	Q9TWK9	Q9twk9 trypanosoma	c 170	3	100.0	22	2	Q8WSF0	Q8wsf0 trichinella
98	3	100.0	19	2	Q97584	Q97584 macaca mula	171	3	100.0	22	2	Q7PDX3	Q7pdx3 anopheles g
99	3	100.0	19	2	Q9TRR6	Q9trr6 oryctolagus	172	3	100.0	22	2	O8HZJ1	O8hzj1 sus scrofa
100	3	100.0	19	2	Q7X8N0	Q7x8n0 zea mays (m	c 173	3	100.0	22	2	Q7M3F1	Q7mf31 bos taurus
101	3	100.0	19	2	Q9S8E9	Q9s8e9 zea mays (m	174	3	100.0	22	2	Q9GM95	Q9gm95 sus scrofa
102	3	100.0	19	2	Q7WVV3	Q7wvv3 streptococc	175	3	100.0	22	2	Q9TRC4	Q9trc4 canis famil
103	3	100.0	19	2	Q9R4T9	Q9r4t9 bacillus th	176	3	100.0	22	2	Q6XEN1	Q6xbn1 pyrrhobryum
104	3	100.0	19	2	Q6LRE8	Q6le88 rattus norv	177	3	100.0	22	2	Q85G98	Q85g98 pyrrhobryum
105	3	100.0	19	2	Q7M068	Q7m068 rattus norv	178	3	100.0	22	2	Q9TC82	Q9tc82 centropomus
c 106	3	100.0	19	2	Q9QV70	Q9qv70 rattus sp.	179	3	100.0	22	2	Q9TC84	Q9tc84 centropomus
107	3	100.0	19	2	Q9PS70	Q9ps70 gallus gall	180	3	100.0	22	2	O42047	O42047 arabidopsis
c 108	3	100.0	19	2	Q905E4	Q905e4 human immun	181	3	100.0	22	2	Q7X8M9	Q7x8m9 zea mays (m
c 109	3	100.0	19	2	Q905F2	Q905f2 human immun	182	3	100.0	22	2	O56233	O56233 thermus aqu
c 110	3	100.0	19	2	Q905G0	Q905g0 human immun	c 183	3	100.0	22	2	Q9R4N9	Q9r4n9 brevundimon
c 111	3	100.0	19	2	Q905G8	Q905g8 human immun	c 184	3	100.0	22	2	O9R4Q3	O9r4q3 pseudomonas
c 112	3	100.0	19	2	Q905H2	Q905h2 human immun	c 185	3	100.0	22	2	O64970	O64970 alfalfa mos
c 113	3	100.0	19	2	Q905I4	Q905i4 human immun	186	3	100.0	22	2	Q87084	Q87084 suid herpes
c 114	3	100.0	19	2	Q905K4	Q905k4 human immun	187	3	100.0	22	2	Q87085	Q87085 suid herpes
c 115	3	100.0	19	2	Q905K8	Q905k8 human immun	c 188	3	100.0	22	2	Q9PXB4	Q9pxb4 duck hepati
c 116	3	100.0	19	2	Q90R11	Q90r11 human immun	189	3	100.0	22	2	O91101	O91101 morone saxa
c 117	3	100.0	20	1	CPBX_CAVPO	P34033 cavia porce	190	3	100.0	23	2	P78489	P78489 homo sapien
c 118	3	100.0	20	1	CK81_THUOB	P80983 thunnus obe	191	3	100.0	23	2	Q9HCW9	Q9hcw9 homo sapien
c 119	3	100.0	20	1	OMP1_ACTAC	P20242 actinobacil	c 192	3	100.0	23	2	Q9UC93	Q9uce3 homo sapien
120	3	100.0	20	1	P33588	P33588 agkistrodon	193	3	100.0	23	2	O25137	O25137 haliotis ru
121	3	100.0	20	2	O8J1R0	O8j1r0 saccharomyc	194	3	100.0	23	2	Q86MM6	Q86mm6 pecten maxi
122	3	100.0	20	2	Q96A79	Q96a79 homo sapien	c 195	3	100.0	23	2	O8MIP9	O8mip9 ovis aries
123	3	100.0	20	2	Q7M4Q3	Q7m4q3 homo sapien	c 196	3	100.0	23	2	O28131	O28131 bos taurus
124	3	100.0	20	2	Q9UCB1	Q9ucb1 homo sapien	c 197	3	100.0	23	2	O9GLD1	O9gld1 bos taurus
c 125	3	100.0	20	2	Q9UC91	Q9uc91 homo sapien	198	3	100.0	23	2	Q6XBM9	Q6xbm9 vittia sali
c 126	3	100.0	20	2	Q9UCR9	Q9ucr9 homo sapien	199	3	100.0	23	2	Q6XBN0	Q6xbn0 vittia sali
127	3	100.0	20	2	O41122	O41122 plasmodium	200	3	100.0	23	2	Q6XBN3	Q6xbn3 vittia pach
128	3	100.0	20	2	O6LBT5	O6lbt5 bos taurus	201	3	100.0	23	2	O8SAB8	O8sabb vittia elim
129	3	100.0	20	2	Q7M3D6	Q7m3d6 equus cabal	202	3	100.0	23	2	O8SAC4	O8sac4 amblystegiu
130	3	100.0	20	2	Q9TQ08	Q9tq08 oryctolagus	c 203	3	100.0	23	2	O6URS8	O6ur88 sorghum bic
131	3	100.0	20	2	Q9TRH8	Q9trh8 oryctolagus	c 204	3	100.0	23	2	Q71V79	Q71v79 arabidopsis
132	3	100.0	20	2	O19618	O19618 homo sapien	205	3	100.0	23	2	Q7X8T2	Q7x8t2 zea mays (m
133	3	100.0	20	2	O19620	O19620 homo sapien	206	3	100.0	23	2	Q9S893	Q9s893 arachis hyp
c 134	3	100.0	20	2	O6URV2	O6urv2 sorghum bic	207	3	100.0	23	2	O9S8G1	O9s8g1 populus tre
135	3	100.0	20	2	Q7X8M7	Q7x8m7 zea mays (m	208	3	100.0	23	2	O50301	O50301 bacillus st
c 136	3	100.0	20	2	Q9R4I9	Q9r4i9 vibrio chol	209	3	100.0	23	2	O6LEQ9	O6leq9 streptococc
137	3	100.0	20	2	Q8K4F4	Q8k4f4 mus musculus	210	3	100.0	23	2	O9AIL1	O9ail1 magnetospir
138	3	100.0	20	2	Q9R2A3	Q9r2a3 mus musculus	211	3	100.0	23	2	O91V21	O91v21 rattus norv
139	3	100.0	20	2	Q9IF53	Q9if53 newcastle d	212	3	100.0	23	2	Q91ZE2	Q91ze2 rattus leuc
140	3	100.0	20	2	Q9PXE4	Q9pxe4 foot-and-mo	213	3	100.0	23	2	O62594	O62594 rattus leuc
141	3	100.0	21	1	GTE2_PSEPU	P82998 pseudomonas	214	3	100.0	23	2	O6LAD4	O6lad4 rattus norv
142	3	100.0	21	2	Q8TDP4	Q8tdp4 homo sapien	215	3	100.0	23	2	Q6S983	Q6s983 suid herpes
143	3	100.0	21	2	Q86UF6	Q86uf6 homo sapien	216	3	100.0	23	2	Q69391	Q69391 suid herpes
144	3	100.0	21	2	Q9P2Z1	Q9p2z1 homo sapien	217	3	100.0	23	2	Q69392	Q69392 suid herpes
c 145	3	100.0	21	2	Q9TR71	Q9tr71 ursus arcto	218	3	100.0	23	2	Q69393	Q69393 suid herpes
146	3	100.0	21	2	Q9T2H2	Q9t2h2 dunaliella	219	3	100.0	23	2	Q69395	Q69395 suid herpes
c 147	3	100.0	21	2	Q41181	Q41181 nicotiana t	220	3	100.0	23	2	Q87078	Q87078 suid herpes
c 148	3	100.0	21	2	Q41559	Q41559 triticum ae	221	3	100.0	23	2	Q87079	Q87079 suid herpes
c 149	3	100.0	21	2	Q41564	Q41564 triticum ae	222	3	100.0	23	2	Q87080	Q87080 suid herpes
c 150	3	100.0	21	2	Q41565	Q41565 triticum ae	223	3	100.0	23	2	Q87081	Q87081 suid herpes
c 151	3	100.0	21	2	Q41566	Q41566 triticum ae	224	3	100.0	23	2	Q87082	Q87082 suid herpes
c 152	3	100.0	21	2	Q42417	Q42417 triticum ae	225	3	100.0	23	2	Q87083	Q87083 suid herpes
c 153	3	100.0	21	2	Q42501	Q42501 triticum ae	226	3	100.0	23	2	Q87086	Q87086 suid herpes
c 154	3	100.0	21	2	Q6URT5	Q6urt5 sorghum bic	c 227	3	100.0	23	1	BOMN_BOMVA	B01505 bombina var
c 155	3	100.0	21	2	Q7X8M8	Q7x8m8 zea mays (m	c 228	3	100.0	24	1	BRIA_RANLU	P82825 rana luteiv
c 156	3	100.0	21	2	Q9S7S6	Q9s7s6 triticum ae	c 229	3	100.0	24	1	B1B1_RANLU	P82826 rana luteiv
c 157	3	100.0	21	2	Q9S8P6	Q9s8p6 pisum sativ	c 230	3	100.0	24	1	CH60_ACICA	P81874 acinetobact
158	3	100.0	21	2	O44611	O44611 buchnera ap	231	3	100.0	24	1	GTE_PSEUF	P82997 pseudomonas
159	3	100.0	21	2	Q79DV3	Q79dv3 escherichia	232	3	100.0	24	2	O6LDJ0	O6ldj0 homo sapien
160	3	100.0	21	2	Q7M123	Q7m123 bacteroides	233	3	100.0	24	2	Q71UK6	Q71uk6 homo sapien
161	3	100.0	21	2	Q9L4S9	Q9l4s9 salmonella	234	3	100.0	24	2	Q7LDT3	Q7ldt3 homo sapien
162	3	100.0	21	2	Q9R4R7	Q9r4r7 streptomyce	235	3	100.0	24	2	Q7Z5M2	Q7z5m2 homo sapien

c 236	3	100.0	24	2	Q658N7	Q658n7 homo sapien	309	3	100.0	25	2	Q9TWN4	Q9twn4 theileria s
c 237	3	100.0	24	2	Q8WT34	Q8wt34 leishmania	310	3	100.0	25	2	Q64FD9	Q64fd9 toxoplasma
c 238	3	100.0	24	2	Q94368	Q94368 caenorhabdi	311	3	100.0	25	2	Q708G1	Q708g1 ovis aries
c 239	3	100.0	24	2	Q7M4H2	Q7m4h2 limulus pol	312	3	100.0	25	2	Q33292	Q33292 zea mays (m
c 240	3	100.0	24	2	Q19654	Q19654 homo sapien	313	3	100.0	25	2	Q76EK5	Q76ek5 auxis roche
c 241	3	100.0	24	2	Q70P01	Q70p01 homo sapien	314	3	100.0	25	2	Q8RV05	Q8rv05 amblystegiu
c 242	3	100.0	24	2	Q7J3FH7	Q7j3fh7 homo sapien	315	3	100.0	25	2	Q8SAC3	Q8sac3 amblystegiu
c 243	3	100.0	24	2	Q9MY32	Q9my32 homo sapien	316	3	100.0	25	2	Q8SAC6	Q8sac6 amblystegiu
c 244	3	100.0	24	2	Q9TNP0	Q9tnp0 homo sapien	317	3	100.0	25	2	Q8SAC8	Q8sac8 amblystegiu
c 245	3	100.0	24	2	Q9TP00	Q9tp00 homo sapien	c 318	3	100.0	25	2	Q6QVF4	Q6qv4 phaseolus v
c 246	3	100.0	24	2	Q9TC80	Q9tc80 homo sapien	c 319	3	100.0	25	2	Q6QVG0	Q6qv0 phaseolus v
c 247	3	100.0	24	2	Q9UQU2	Q9uqu2 homo sapien	c 320	3	100.0	25	2	Q6QVG3	Q6qv3 phaseolus v
c 248	3	100.0	24	2	Q79910	Q79910 chamaeleo f	c 321	3	100.0	25	2	Q6QVG9	Q6qv9 phaseolus v
c 249	3	100.0	24	2	Q8SH84	Q8sh84 brookesia t	c 322	3	100.0	25	2	Q6QVH7	Q6qv7 phaseolus v
c 250	3	100.0	24	2	Q8SH89	Q8sh89 brookesia t	c 323	3	100.0	25	2	Q6QVI2	Q6qv12 phaseolus v
c 251	3	100.0	24	2	Q8SH95	Q8sh95 brookesia p	c 324	3	100.0	25	2	Q6QVI8	Q6qv18 phaseolus v
c 252	3	100.0	24	2	Q8SH91	Q8sh91 brookesia n	c 325	3	100.0	25	2	Q6QVJ9	Q6qv19 phaseolus v
c 253	3	100.0	24	2	Q8SHB0	Q8shb0 rhampholeon	c 326	3	100.0	25	2	Q6QVK4	Q6qv4 phaseolus v
c 254	3	100.0	24	2	Q8SHB6	Q8shb6 furcifer ve	327	3	100.0	25	2	Q9AT69	Q9at69 coffea arab
c 255	3	100.0	24	2	Q8SHB9	Q8shb9 furcifer ou	328	3	100.0	25	2	Q44606	Q44606 buchnera ap
c 256	3	100.0	24	2	Q8SHC2	Q8shc2 furcifer la	329	3	100.0	25	2	Q6WVH1	Q6wvh1 actinomadar
c 257	3	100.0	24	2	Q8SHC5	Q8shc5 furcifer la	330	3	100.0	25	2	Q7DJ11	Q7dj11 salmonella
c 258	3	100.0	24	2	Q8SHC8	Q8shc8 furcifer be	331	3	100.0	25	2	Q7M0X0	Q7m0x0 streptomyc
c 259	3	100.0	24	2	Q8SHD1	Q8shd1 furcifer ba	332	3	100.0	25	2	Q840F9	Q840f9 chlamydia t
c 260	3	100.0	24	2	Q8SHD4	Q8shd4 chamaeleo w	333	3	100.0	25	2	Q9S0U6	Q9s0u6 shigella so
c 261	3	100.0	24	2	Q8SHE6	Q8she6 chamaeleo q	334	3	100.0	25	2	P72429	P72429 salmonella
c 262	3	100.0	24	2	Q8SHE9	Q8she9 chamaeleo p	335	3	100.0	25	2	Q7DAR1	Q7dar1 salmonella
c 263	3	100.0	24	2	Q8SHF2	Q8shf2 chamaeleo n	c 336	3	100.0	25	2	Q62533	Q62533 mus spretus
c 264	3	100.0	24	2	Q8SHF5	Q8shf5 chamaeleo m	337	3	100.0	25	2	Q71V84	Q71v84 mus musculu
c 265	3	100.0	24	2	Q8SHF8	Q8shf8 chamaeleo m	338	3	100.0	25	2	Q9JXY4	Q9jxy4 mus musculu
c 266	3	100.0	24	2	Q8SHG1	Q8shg1 chamaeleo j	339	3	100.0	25	2	Q80J43	Q80j43 oyster noro
c 267	3	100.0	24	2	Q8SHG4	Q8shg4 chamaeleo j	340	3	100.0	25	2	Q80J44	Q80j44 oyster noro
c 268	3	100.0	24	2	Q8SHH3	Q8shh3 chamaeleo f	341	3	100.0	25	2	Q80J46	Q80j46 oyster noro
c 269	3	100.0	24	2	Q8SHH6	Q8shh6 chamaeleo f	c 342	3	100.0	25	2	Q9UWG7	Q9uwg7 sulfolobus
c 270	3	100.0	24	2	Q8SHI2	Q8shi2 chamaeleo d	343	3	100.0	26	2	Q8ZV3	Q8zv3 pyrobaculum
c 271	3	100.0	24	2	Q8SHI5	Q8shi5 chamaeleo c	344	3	100.0	26	2	Q9HFN6	Q9hfn6 candida rug
c 272	3	100.0	24	2	Q8SHJ7	Q8shj7 calumma par	345	3	100.0	26	2	Q6LDI0	Q6ldi0 homo sapien
c 273	3	100.0	24	2	Q8SHK0	Q8shk0 calumma osh	346	3	100.0	26	2	Q9NP34	Q9np34 homo sapien
c 274	3	100.0	24	2	Q8SHK3	Q8shk3 calumma nas	c 347	3	100.0	26	2	Q77226	Q77226 helix asper
c 275	3	100.0	24	2	Q8SHK6	Q8shk6 calumma hil	348	3	100.0	26	2	P90723	P90723 berce ovata
c 276	3	100.0	24	2	Q8SHK9	Q8shk9 calumma glo	c 349	3	100.0	26	2	Q9BLZ9	Q9blz9 macrotrache
c 277	3	100.0	24	2	Q8SHL5	Q8shl5 calumma fur	350	3	100.0	26	2	Q9NBB1	Q9nbb1 drosophila
c 278	3	100.0	24	2	Q8SHL8	Q8shl8 calumma cuc	351	3	100.0	26	2	Q64FE3	Q64fe3 toxoplasma
c 279	3	100.0	24	2	Q8SHM1	Q8shm1 calumma bre	c 352	3	100.0	26	2	Q8SP22	Q8sp22 macaca mula
c 280	3	100.0	24	2	Q8SHM4	Q8shm4 calumma boe	353	3	100.0	26	2	Q79883	Q79883 anolis pate
c 281	3	100.0	24	2	Q8SHM7	Q8shm7 bradypodion	354	3	100.0	26	2	P92614	P92614 aspidosceli
c 282	3	100.0	24	2	Q8SHN0	Q8shn0 bradypodion	355	3	100.0	26	2	P92652	P92652 euprepis au
c 283	3	100.0	24	2	Q8SHN3	Q8shn3 bradypodion	356	3	100.0	26	2	P92772	P92772 xantusia ar
c 284	3	100.0	24	2	Q8SHN6	Q8shn6 bradypodion	357	3	100.0	26	2	Q8SIU0	Q8siu0 xantusia ar
c 285	3	100.0	24	2	Q8SHN9	Q8shn9 bradypodion	358	3	100.0	26	2	Q8SIU3	Q8siu3 xantusia be
c 286	3	100.0	24	2	Q8SHP2	Q8shp2 bradypodion	359	3	100.0	26	2	Q8SIU6	Q8siu6 xantusia he
c 287	3	100.0	24	2	Q8SK10	Q8sk10 furcifer ca	360	3	100.0	26	2	Q6WBP2	Q6wbp2 scelopor
c 288	3	100.0	24	2	Q38270	Q38270 bacterioph	361	3	100.0	26	2	Q6WBS2	Q6wbs2 scelopor
c 289	3	100.0	24	2	Q8SAC1	Q8sac1 amblystegiu	362	3	100.0	26	2	Q6WBX3	Q6wbx3 phrynosoma
c 290	3	100.0	24	2	Q8SAC7	Q8sac7 amblystegiu	363	3	100.0	26	2	Q71DS0	Q71ds0 leioccephalu
c 291	3	100.0	24	2	Q6K426	Q6k426 oryza sativ	364	3	100.0	26	2	Q71DY3	Q71dy3 prietadacty
c 292	3	100.0	24	2	Q6URS9	Q6urs9 sorghum bic	365	3	100.0	26	2	Q71DZ2	Q71dz2 diplolaemus
c 293	3	100.0	24	2	Q9SRG2	Q9srg2 maclura pom	366	3	100.0	26	2	Q71DZ5	Q71dz5 diplolaemus
c 294	3	100.0	24	2	Q8RIC0	Q8ric0 fusobacteri	367	3	100.0	26	2	Q71DZ8	Q71dz8 anolis sagr
c 295	3	100.0	24	2	Q9PBP9	Q9pbp9 mus musculu	368	3	100.0	26	2	Q71E04	Q71e04 anolis diet
c 296	3	100.0	24	2	Q7TQ64	Q7tq64 mus musculu	369	3	100.0	26	2	Q71E07	Q71e07 anolis cris
c 297	3	100.0	24	2	Q69137	Q69137 human herpe	370	3	100.0	26	2	Q71E10	Q71e10 anolis cybo
c 298	3	100.0	24	2	Q788Q0	Q788q0 xenopus lae	371	3	100.0	26	2	Q71E16	Q71e16 brachylophu
c 299	3	100.0	25	2	Q7M4X3	Q7m4x3 acromonium	372	3	100.0	26	2	Q71E25	Q71e25 corytophane
c 300	3	100.0	25	2	Q9GQ67	Q9gq67 homo sapien	373	3	100.0	26	2	Q71ESE4	Q71ese4 phymaturus
c 301	3	100.0	25	2	Q9UCR8	Q9ucr8 homo sapien	374	3	100.0	26	2	Q71ESE7	Q71ese7 phymaturus
c 302	3	100.0	25	2	Q9UL44	Q9ul44 homo sapien	375	3	100.0	26	2	Q76EJ9	Q76ej9 auxis roche
c 303	3	100.0	25	2	Q8IA15	Q8ia15 perionyx ex	376	3	100.0	26	2	Q85C11	Q85c11 pyrrhobryum
c 304	3	100.0	25	2	Q8MWU6	Q8mwu6 eisenia and	377	3	100.0	26	2	Q85C12	Q85c12 pyrrhobryum
c 305	3	100.0	25	2	Q8SZG6	Q8szg6 drosophila	378	3	100.0	26	2	Q85CJ7	Q85cj7 pyrrhobryum
c 306	3	100.0	25	2	Q9BME0	Q9bme0 sagitta sp.	379	3	100.0	26	2	Q85G89	Q85g89 pyrrhobryum
c 307	3	100.0	25	2	Q9TWE4	Q9twe4 lumbricus t	380	3	100.0	26	2	Q85G93	Q85g93 pyrrhobryum
c 308	3	100.0	25	2	Q9TWI1	Q9twi1 aplysia cal	381	3	100.0	26	2	Q9T8X9	Q9t8x9 phymaturus

382	3	100.0	26	2	Q9ZVS8	Q9ZV88	stenocercus	455	3	100.0	27	2	O19703	019703	homo sapien
383	3	100.0	26	2	Q9ZVT1	Q9ZVT1	phymaturus	456	3	100.0	27	2	Q67A92	Q67A92	homo sapien
384	3	100.0	26	2	Q9ZVT4	Q9ZVT4	leioccephalu	457	3	100.0	27	2	Q67A93	Q67A93	homo sapien
385	3	100.0	26	2	Q8RV97	Q8RV97	amblystegiu	458	3	100.0	27	2	Q67A94	Q67A94	homo sapien
386	3	100.0	26	2	Q8SAC5	Q8SAC5	amblystegiu	459	3	100.0	27	2	Q67A95	Q67A95	homo sapien
387	3	100.0	26	2	Q8SAD0	Q8SAD0	amblystegiu	460	3	100.0	27	2	Q67A96	Q67A96	homo sapien
388	3	100.0	26	2	Q8SAD1	Q8SAD1	amblystegiu	461	3	100.0	27	2	Q67A97	Q67A97	homo sapien
389	3	100.0	26	2	Q8SAD5	Q8SAD5	amblystegiu	462	3	100.0	27	2	Q67A98	Q67A98	homo sapien
390	3	100.0	26	2	Q9RSF2	Q9RSF2	thiobacillu	463	3	100.0	27	2	Q67A99	Q67A99	homo sapien
391	3	100.0	26	2	Q9Z424	Q9Z424	pseudomonas	464	3	100.0	27	2	Q67AA0	Q67AA0	homo sapien
392	3	100.0	26	2	Q63408	Q63408	rattus norv	465	3	100.0	27	2	Q67AA1	Q67AA1	homo sapien
393	3	100.0	26	2	Q6LCB3	Q6LCB3	mus muscucu	466	3	100.0	27	2	Q67AA2	Q67AA2	homo sapien
394	3	100.0	26	2	Q6LCE0	Q6LCE0	mus muscucu	467	3	100.0	27	2	Q67AA3	Q67AA3	homo sapien
395	3	100.0	26	2	Q6LEI5	Q6LEI5	rattus norv	468	3	100.0	27	2	Q67AA4	Q67AA4	homo sapien
396	3	100.0	26	2	Q9QVG9	Q9QVG9	rattus sp.	469	3	100.0	27	2	Q67AA5	Q67AA5	homo sapien
397	3	100.0	26	2	Q788Q1	Q788Q1	xenopus lae	470	3	100.0	27	2	Q67AA6	Q67AA6	homo sapien
398	3	100.0	26	2	Q8AWR9	Q8AWR9	stomatohin	471	3	100.0	27	2	Q67AA7	Q67AA7	homo sapien
399	3	100.0	26	2	Q8AWS0	Q8AWS0	stomatohin	472	3	100.0	27	2	Q67AA8	Q67AA8	homo sapien
400	3	100.0	26	2	Q8AWS1	Q8AWS1	stomatohin	473	3	100.0	27	2	Q67AA9	Q67AA9	homo sapien
401	3	100.0	26	2	Q8AWS2	Q8AWS2	pollimyrus	474	3	100.0	27	2	Q67AB0	Q67AB0	homo sapien
402	3	100.0	26	2	Q8AWS3	Q8AWS3	pollimyrus	475	3	100.0	27	2	Q67AB1	Q67AB1	homo sapien
403	3	100.0	26	2	Q8AWS4	Q8AWS4	pollimyrus	476	3	100.0	27	2	Q67AB2	Q67AB2	homo sapien
404	3	100.0	26	2	Q8AWS5	Q8AWS5	pollimyrus	477	3	100.0	27	2	Q67AB3	Q67AB3	homo sapien
405	3	100.0	26	2	Q8AWS6	Q8AWS6	pollimyrus	478	3	100.0	27	2	Q67AB4	Q67AB4	homo sapien
406	3	100.0	26	2	Q8AWS7	Q8AWS7	paramomyro	479	3	100.0	27	2	Q67AB5	Q67AB5	homo sapien
407	3	100.0	26	2	Q8AWS8	Q8AWS8	myomyrus ma	480	3	100.0	27	2	Q67AB6	Q67AB6	homo sapien
408	3	100.0	26	2	Q8AWS9	Q8AWS9	mormyrus ru	481	3	100.0	27	2	Q67AB7	Q67AB7	homo sapien
409	3	100.0	26	2	Q8AWT0	Q8AWT0	mormyrus ov	482	3	100.0	27	2	Q67AB8	Q67AB8	homo sapien
410	3	100.0	26	2	Q8AWT1	Q8AWT1	mormyrops m	483	3	100.0	27	2	Q67AB9	Q67AB9	homo sapien
411	3	100.0	26	2	Q8AWT2	Q8AWT2	mormyrops z	484	3	100.0	27	2	Q67AC0	Q67AC0	homo sapien
412	3	100.0	26	2	Q8AWT3	Q8AWT3	mormyrops n	485	3	100.0	27	2	Q67AC1	Q67AC1	homo sapien
413	3	100.0	26	2	Q8AWT4	Q8AWT4	marcusenius	486	3	100.0	27	2	Q67AC2	Q67AC2	homo sapien
414	3	100.0	26	2	Q8AWT5	Q8AWT5	marcusenius	487	3	100.0	27	2	Q67AC3	Q67AC3	homo sapien
415	3	100.0	26	2	Q8AWT6	Q8AWT6	marcusenius	488	3	100.0	27	2	Q67AC4	Q67AC4	homo sapien
416	3	100.0	26	2	Q8AWT7	Q8AWT7	marcusenius	489	3	100.0	27	2	Q79886	Q79886	basiliscus
417	3	100.0	26	2	Q8AWT8	Q8AWT8	marcusenius	490	3	100.0	27	2	Q79889	Q79889	crotaphytus
418	3	100.0	26	2	Q8AWT9	Q8AWT9	ivindomyrus	491	3	100.0	27	2	Q79892	Q79892	gambelia wi
419	3	100.0	26	2	Q8AWU0	Q8AWU0	ischthyis h	492	3	100.0	27	2	Q79895	Q79895	hoplocercus
420	3	100.0	26	2	Q8AWU1	Q8AWU1	hippopotamy	493	3	100.0	27	2	Q79898	Q79898	liolaemus p
421	3	100.0	26	2	Q8AWU2	Q8AWU2	hyperopisus	494	3	100.0	27	2	Q79901	Q79901	opliurus cuv
422	3	100.0	26	2	Q8AWU3	Q8AWU3	hippopotamy	495	3	100.0	27	2	Q79904	Q79904	phrynosoma
423	3	100.0	26	2	Q8AWU4	Q8AWU4	hippopotamy	496	3	100.0	27	2	Q79907	Q79907	saurosoma
424	3	100.0	26	2	Q8AWU5	Q8AWU5	gnathonemus	497	3	100.0	27	2	P92574	P92574	bipes bipor
425	3	100.0	26	2	Q8AWU6	Q8AWU6	genyomyrus	498	3	100.0	27	2	P92630	P92630	eremias gra
426	3	100.0	26	2	Q8AWU7	Q8AWU7	campylomorm	499	3	100.0	27	2	P92705	P92705	platysaurus
427	3	100.0	26	2	Q8AWU8	Q8AWU8	campylomorm	500	3	100.0	27	2	Q8W7G5	Q8W7G5	liolaemus m
428	3	100.0	26	2	Q8AWU9	Q8AWU9	campylomorm								
429	3	100.0	26	2	Q8AWV0	Q8AWV0	campylomorm								
430	3	100.0	26	2	Q8AWV1	Q8AWV1	brienomyrus								
431	3	100.0	26	2	Q8AWV2	Q8AWV2	brienomyrus								
432	3	100.0	26	2	Q8AWV3	Q8AWV3	brienomyrus								
433	3	100.0	26	2	Q8AWV4	Q8AWV4	brienomyrus								
434	3	100.0	26	2	Q8AWV5	Q8AWV5	brienomyrus								
435	3	100.0	26	2	Q8AWV6	Q8AWV6	boulengerom								
436	3	100.0	26	2	Q8AWV7	Q8AWV7	fucus vesic								
437	3	100.0	27	1	PSBY_FUCVE	PSBY_FUCVE	desulfovibr								
438	3	100.0	27	1	SODM_DSDE	SODM_DSDE	neurospora								
439	3	100.0	27	2	Q7SEU3	Q7SEU3	homo sapien								
440	3	100.0	27	2	Q8WTR6	Q8WTR6	homo sapien								
441	3	100.0	27	2	Q965Q2	Q965Q2	homo sapien								
442	3	100.0	27	2	Q72700	Q72700	homo sapien								
443	3	100.0	27	2	Q9BS88	Q9BS88	homo sapien								
444	3	100.0	27	2	Q9UEF5	Q9UEF5	homo sapien								
445	3	100.0	27	2	Q96889	Q96889	sacculina c								
446	3	100.0	27	2	Q25584	Q25584	oikopleura								
447	3	100.0	27	2	Q8MTK5	Q8MTK5	aurelia aur								
448	3	100.0	27	2	Q94448	Q94448	chaetopteru								
449	3	100.0	27	2	Q69H26	Q69H26	symagittif								
450	3	100.0	27	2	Q7RBB1	Q7RBB1	plasmodium								
451	3	100.0	27	2	Q9BME3	Q9BME3	oxytricha t								
452	3	100.0	27	2	Q9Y181	Q9Y181	priapulius c								
453	3	100.0	27	2	Q29019	Q29019	sus scrofa								
454	3	100.0	27	2	Q9WZR2	Q9WZR2	oryctolagus								
455	3	100.0	27	2	O19501	O19501	homo sapien								

## ALIGNMENTS

RESULT 1  
 RS1\_ERWCH  
 ID RS1\_ERWCH STANDARD; PRT; 8 AA.  
 AC P37985;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE 30S ribosomal protein S1 (Fragment).  
 GN Name=rpS8;  
 OS Erwinia chrysanthemi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Pectobacterium.  
 OX NCBI\_TaxID=556;  
 RN [1]  
 RC STRAIN=3937;  
 RL Doullie A., Toussaint A., Faelen M.;  
 CC Submitted (AUG-1993) to the EMBL/Genbank/DBJ databases.  
 CC -!- FUNCTION: Binds mRNA; thus facilitating recognition of the  
 CC initiation point. It is needed to translate mRNA with a short  
 CC Shine-Dalgarno (SD) purine-rich sequence (By similarity).  
 CC -!- SIMILARITY: Belongs to the ribosomal protein S1P family.  
 CC -----

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DR EMBL; X74750; CAA52769.1; -;  
DR PIR; S37141; S37141.  
KW Repeat; Ribosomal protein; RNA-binding.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Alignment Scores:  
Pred. No.: 1.28e+08 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-070-588a-112 (1-11) x RS1\_ERWCH (1-8)

OY 10 AGTGCCAAA 2  
Db 4 SerAlaLys 6  
RESULT 2  
Q6JC68 PRELIMINARY; PRT; 8 AA.  
ID Q6JC68  
AC Q6JC68;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Isoflavone synthase 1 (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15356384;  
RA Subramanian S., Hu X., Lu G., Odell J.T., Yu O.;  
RT "The promoters of two isoflavone synthase genes respond differentially  
RT to modulation and defense signals in transgenic soybean roots.";  
RL Plant Mol. Biol. 54:623-639(2004).  
DR EMBL; AY530096; AAT01227.1; -;  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 859 MW; F1772DD72B172726 CRC64;

Alignment Scores:  
Pred. No.: 1.28e+08 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q6JC68 (1-8)

OY 3 TTGGCACTA 11  
Db 5 LeuAlaLeu 7  
RESULT 3  
Q9MW43 PRELIMINARY; PRT; 9 AA.  
ID Q9MW43  
AC Q9MW43;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MHC class I antigen (Fragment).  
GN Name=HLA-B39061;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Blood;  
RX MEDLINE=97246738; PubMed=9089103; DOI=10.1007/s002510050227;  
RA Vargas-Alarcon G., Gomez-Casado E., Martinez-Laso J., Granados J.,  
RA Layrisse Z., Alegre R., Arnaliz-Villena A.;  
RT "Differences in intron 2 sequences between B\*39061 and B\*39062 in  
RT Amerindians: comparison with those of B\*3901, B\*5101, and B\*52012  
RT alleles.";  
RL Immunogenetics 45:436-439(1997).  
DR EMBL; L76640; AAP86298.1; -;  
DR GO; GO:0030106; F:MHC class I receptor activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
FT NON\_TER 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 975 MW; 51C661AB01A72DD7 CRC64;

Alignment Scores:  
Pred. No.: 1.14e+08 Length: 9  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q9MW43 (1-9)

OY 3 TTGGCACTA 11  
Db 2 LeuAlaLeu 4  
RESULT 4  
CX81 CANFA STANDARD; PRT; 10 AA.  
ID CX81 CANFA  
AC P61504;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIII-heart (EC 1.9.3.1) (Cytochrome c  
DE oxidase subunit 8-1) (Fragment).  
GN Name=COX8H;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Heart, and Liver;  
RX MEDLINE=96092035; PubMed=8529022; DOI=10.1016/0305-0491(95)00093-3;  
RA Linder D., Freund R., Kadenbach B.;  
RT "Species-specific expression of cytochrome c oxidase isozymes.";  
RL Comp. Biochem. Physiol. 112B:461-469(1995).  
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide  
CC chains of cytochrome c oxidase, the terminal oxidase in  
CC mitochondrial electron transport.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
CC -!- TISSUE SPECIFICITY: Heart specific isoform.  
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.  
KW Direct protein sequencing; Inner membrane; Mitochondrion;  
KW Oxidoreductase.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1027 MW; C22AFFB40DC7633D CRC64;  
Alignment Scores:  
Pred. No.: 4.93e+05 Length: 10

Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x CX81\_CANFA (1-10)

QY 10 AGTGCCAAA 2  
Db 2 SerAlaLys 4

RESULT 5  
Q50843 PRELIMINARY; PRT; 10 AA.

ID Q50843  
AC Q50843  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE RNA polymerase gene 3', flanking region with AT-rich DNA sequence (Fragment).  
DE Methanococcus voltae.  
OS Methanococcus voltae.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanococcaceae; Methanococcus.  
OX NCBI\_TaxID=2188;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85230552; PubMed=4006907;  
RA Bolischweiler C., Kuehn R., Klein A.;  
RT "Non-repetitive AT-rich sequences are found in intergenic regions of  
RT Methanococcus voltae DNA."  
RL EMBO J. 4:805-809(1985).  
DR EMBL; X02517; CAA26353.1; --  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1149 MW; 27F22A2772CAA9C8 CRC64;

Alignment Scores:  
Pred. No.: 4.93e+05 Length: 10  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q50843 (1-10)

QY 9 GTCGCAAG 1  
Db 6 ValProLys 8

RESULT 6  
Q7S225 PRELIMINARY; PRT; 10 AA.

ID Q7S225  
AC Q7S225  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DE Predicted protein.  
DE Name=NCU09889.1;  
GN Neurospora crassa.  
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=OR74A;  
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,  
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
RA Sellitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
RA Kotne G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Kamal M., Kamysseelis M., Mauceli E., Bialke C., Rudd S., Frishman D.,  
RA Krystofova S., Raemussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,  
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
RA Natvig D.O., Alex L.A., Maunhaupt G., Ebbole D.J., Freitag M.,  
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,  
RL Nature 0:0-0(2003).  
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AABX01000434; EAA29420.1; --  
SQ SEQUENCE 10 AA; 1071 MW; DA471E27272DD732 CRC64;

Alignment Scores:  
Pred. No.: 4.93e+05 Length: 10  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7S225 (1-10)

QY 3 TTGGCACTA 11  
Db 4 LeuAlaLeu 6

RESULT 7  
Q95M70 PRELIMINARY; PRT; 10 AA.

ID Q95M70  
AC Q95M70  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Beta-2 microglobulin (Fragment).  
GN Name=B2MG;  
OS Trichosurus vulpecula (Brush-tailed possum).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.  
OX NCBI\_TaxID=9337;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22419909; PubMed=12531282; DOI=10.1016/S0161-5890(02)00260-2;  
RA Western A.H., Eckery D.C., Demmer J., Juengel J.L., McNatty K.P.,  
RA Fidler A.E.;  
RT "Expression of the FcRn receptor (alpha and beta) gene homologues in  
RT the intestine of suckling brushtail possum (Trichosurus vulpecula)  
RT pouch young.";  
RL Mol. Immunol. 39:707-717(2003).  
DR EMBL; AY033330; AAK57520.1; --  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1179 MW; CD4BEE2059C0440D CRC64;

Alignment Scores:  
Pred. No.: 4.93e+05 Length: 10  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q95M70 (1-10)

QY 3 TTGGCACTA 11  
Db 8 LeuAlaLeu 10

RESULT 8  
Q8SAC2 PRELIMINARY; PRT; 10 AA.

ID Q8SAC2  
AC Q8SAC2;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE AtPB (Fragment).  
OS Amblystegium varium.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.  
OX NCBI\_TaxID=111436;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15062791; DOI=10.1016/j.ympev.2003.09.020;  
RA Vanderpoorten A., Shaw A.J., Cox C.J.;  
RT "Evolution of multiple paralogous adenosine kinase genes in the moss  
RT genus Hygroamblystegium: phylogenetic implications.";  
RL Mol. Phylogenet. Evol. 31:505-516(2004).  
DR EMBL; AF464972; AAL75469.1; -;  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1143 MW; 9D5040D1B415BAB1 CRC64;

Alignment Scores:  
Pred. No.: 4.93e+05 Length: 10  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x QBSAC2 (1-10)

QY 2 TTGGCACT 10  
Db 8 PheGlyThr 10

RESULT 9

Q9S905 PRELIMINARY; PRT; 10 AA.

ID Q9S905  
AC Q9S905;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE S3 peptide (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=92232221; PubMed=1368037; DOI=10.1016/0031-9422(92)80003-W;  
RA Hirano H., Kagawa H., Okubo K.;  
RL Phytochemistry 31:731-735(1992).

FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 975 MW; 3C733271A879D1B7 CRC64;

Alignment Scores:  
Pred. No.: 4.93e+05 Length: 10  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9S905 (1-10)

QY 2 TTGGCACT 10  
Db 5 PheGlyThr 7

RESULT 10

Q9C1R7 PRELIMINARY; PRT; 11 AA.  
AC Q9C1R7

DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Ssulp (Fragment).  
GN Name=ssul;  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=RT73;  
RC MEDLINE=22253762; PubMed=12368245; DOI=10.1101/gr.436602;  
RA Perez-Ortin J.E., Querol A., Puig S., Barrio E.;  
RT "Molecular Characterization of a Chromosomal Rearrangement Involved in  
RT the Adaptive Evolution of Yeast Strains.";  
RL Genome Res. 12:1533-1539(2002).  
DR EMBL; AF239758; AAK15080.1; -;  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1274 MW; 12567614D732D374 CRC64;

Alignment Scores:  
Pred. No.: 4.79e+05 Length: 11  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9C1R7 (1-11)

QY 3 TTGGCACTA 11  
Db 7 LeuAlaLeu 9

RESULT 11

Q7M374 PRELIMINARY; PRT; 11 AA.

ID Q7M374  
AC Q7M374;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Ribosomal protein MRP-S24, mitochondrial (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.

RA Graack H.R.;  
RL Submitted (JUL-1999) to the PIR data bank.  
DR PIR; S78765; S78765.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1264 MW; 95F49156A32772CA CRC64;

Alignment Scores:  
Pred. No.: 4.79e+05 Length: 11  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7M374 (1-11)

QY 9 GTGCCAAAG 1  
Db 5 ValProLys 7

RESULT 12

Q9UEX7

```
ID Q9UEX7 PRELIMINARY; PRT; 11 AA.
AC Q9UEX7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Leucocyte antigen B (Fragment).
GN Names=HLA-A*03;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fae I., Kriks D., Cernava B., Fischer G.F.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY622283; CAB65736.1; -
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1118 MW; 5191BC69C1A72DD7 CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q9UEX7 (1-11)
QY 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 13
Q68QV9 PRELIMINARY; PRT; 11 AA.
AC Q68QV9;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Arginine biosynthesis repressor (Fragment).
GN Name=argR;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15322001; DOI=10.1128/IAI.72.9.5080-5088.2004;
RA Lan R., Alles M.C., Donohoe K., Martinez M.B., Reeves P.R.;
RT "Molecular evolutionary relationships of enteroinvasive Escherichia
colli and Shigella spp.";
RL Infect. Immun. 72:5080-5088(2004).
DR EMBL; AY627168; AAU01857.1; -
DR EMBL; AY627169; AAU01859.1; -
DR EMBL; AY627170; AAU01861.1; -
DR EMBL; AY627171; AAU01863.1; -
DR EMBL; AY627172; AAU01865.1; -
DR EMBL; AY627173; AAU01867.1; -
DR EMBL; AY627174; AAU01869.1; -
DR EMBL; AY627175; AAU01871.1; -
DR EMBL; AY627176; AAU01873.1; -
DR EMBL; AY627177; AAU01875.1; -
DR EMBL; AY627178; AAU01877.1; -
DR EMBL; AY627244; AAU01795.1; -
DR EMBL; AY627245; AAU01797.1; -
DR EMBL; AY627246; AAU01799.1; -
DR EMBL; AY627247; AAU01801.1; -
DR EMBL; AY627248; AAU01803.1; -
DR EMBL; AY627249; AAU01805.1; -
DR EMBL; AY627250; AAU01807.1; -
DR EMBL; AY627251; AAU01809.1; -
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DR EMBL; AY627252; AAU01811.1; -
DR EMBL; AY627253; AAU01813.1; -
DR EMBL; AY627254; AAU01815.1; -
DR EMBL; AY627255; AAU01817.1; -
DR EMBL; AY627256; AAU01819.1; -
DR EMBL; AY627257; AAU01821.1; -
DR EMBL; AY627258; AAU01823.1; -
DR EMBL; AY627259; AAU01825.1; -
DR EMBL; AY627260; AAU01827.1; -
DR EMBL; AY627261; AAU01829.1; -
DR EMBL; AY627262; AAU01831.1; -
DR EMBL; AY627263; AAU01833.1; -
DR EMBL; AY627264; AAU01835.1; -
DR EMBL; AY627265; AAU01837.1; -
DR EMBL; AY627266; AAU01839.1; -
DR EMBL; AY627267; AAU01841.1; -
DR EMBL; AY627268; AAU01843.1; -
DR EMBL; AY627269; AAU01845.1; -
DR EMBL; AY627270; AAU01847.1; -
DR EMBL; AY627271; AAU01849.1; -
DR EMBL; AY627272; AAU01851.1; -
DR EMBL; AY627273; AAU01853.1; -
DR EMBL; AY627167; AAU01855.1; -
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1277 MW; 9B5PBE2206D33DC5 CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q68QV9 (1-11)
QY 10 AGTGCAAA 2
Db 4 SerAlaLys 6

RESULT 14
Q7MOD4 PRELIMINARY; PRT; 11 AA.
AC Q7MOD4;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cytochrome-c oxidase (EC 1.9.3.1) chain Via-H, cardiac
(Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR PIR; S65377; S65377.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 927 MW; 4F3E577D71EAA873 CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
```



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US-10-070-588A-112 (1-11) x Q7M0D4 (1-11)
QY 10 AGTGCCAAA 2
Db 2 SerAlaLys 4

RESULT 15
Q84247
ID Q84247 PRELIMINARY; PRT; 11 AA.
AC Q84247;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Capsid protein VP2 (Fragment).
OS Polyomavirus BK (BKV).
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10629;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gardner;
RX MEDLINE=90324932; PubMed=21651132;
RA Moens U., Sundsfjord A., Flegstad T., Traavik T.;
RT "BK virus early RNA transcripts in stably transformed cells : enhanced
RT levels induced by dibutyl cAMP, forskolin and 12-O-
RT tetradecanoylphorbol-13-acetate treatment.";
RL J. Gen. Virol. 71:1461-1471(1990).
DR EMBL; D00678; BAA00585.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1044 MW; C2786C4E272DD72D CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q84247 (1-11)
QY 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7

RESULT 16
TKN_KASSE
ID TKN_KASSE STANDARD; PRT; 12 AA.
AC P08611;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kassinin.
OS Kassina senegalensis (Senegal running frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina
OX NCBI_TaxID=8415;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=77246385; PubMed=891753;
RA Anastasi A., Montecucchi P.C., Erpamer V., Visser J.;
RT "Amino acid composition and sequence of kassinin, a tachykinin
RT dodecapeptide from the skin of the African frog Kassina
RT senegalensis.";
RL Experientia 33:857-858(1977).
CC -|- FUNCTION: Tachykines are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
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CC -|- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S07206; S07206.
DR PDB; 1MYU; NMR; A=1-12.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW 3D-structure; Amidation; Amphibian defense peptide;
KW Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD_RES 12 12 Methionine amide.
SQ SEQUENCE 12 AA; 1336 MW; 91757AB9DD6DAB5 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x TKN_KASSE (1-12)
QY 9 GTGCCAAAG 1
Db 2 ValProLys 4

RESULT 17
Q8J0A7
ID Q8J0A7 PRELIMINARY; PRT; 12 AA.
AC Q8J0A7;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE SSU1 protein (Fragment).
CN Name=SSU1;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 10557; and CECT 10120;
RX MEDLINE=22253762; PubMed=12368245; DOI=10.1101/gr.436602;
RA Perez-Ortin J.E., Querol A., Puig S., Barrio E.;
RT "Molecular Characterization of a Chromosomal Rearrangement Involved in
RT the Adaptive Evolution of Yeast Strains.";
RL Genome Res. 12:1533-1539(2002).
DR EMBL; AJ458364; CAD30222.1; -.
DR EMBL; AJ458366; CAD30224.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1402 MW; 3162567614D732D3 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q8J0A7 (1-12)
QY 3 TTGGCACTA 11
Db 7 LeuAlaLeu 9

RESULT 18
Q7M4X9
ID Q7M4X9 PRELIMINARY; PRT; 12 AA.
AC Q7M4X9;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Ribosomal protein S3 (Fragment).
```

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OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Chow L.P., Fukaya N., Sugura Y., Ueno Y., Tabuchi K., Teugita A.;
RL Submitted (OCT-1994) to the PIR data bank.
DR PIR; PA0098; PA0098.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1242 MW; 227EFCBA7C2772D7 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7M4X9 (1-12)

QY 9 GTGCCAAG 1
Db 6 ValProLys 8

RESULT 19
Q96PHO PRELIMINARY; PRT; 12 AA.
ID Q96PHO;
AC Q96PHO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE H1028 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21474610; PubMed=11590366;
RA Demirci F.Y., White N.J., Rigatti B.W., Lewis K.F., Gorin M.B.;
RT "Identification, genomic structure, and screening of the vacuolar
RT proton-ATPase membrane sector-associated protein M8-9 gene within the
RT COD1 critical region (Xp11.4).";
RL Mol. Vision 7:234-239 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Demirci F.Y., White N.J., Rigatti B.W., Chun-Fang X., Gorin M.B.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354120; AAL11062.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1246 MW; D55E1977EE2732D2 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q96PHO (1-12)

QY 3 TTGGCACTA 11
Db 8 LeuAlaLeu 10

RESULT 20
Q31851 PRELIMINARY; PRT; 12 AA.
ID Q31851;
AC Q31851;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia; TISSUE=Leaf;
RX MEDLINE=94187724; PubMed=8139555;
RA Conley T.R., Park S.-C., Kwon H.-S., Peng H.-S., Shih M.-C.;
RT "Characterization of cis-acting elements in light regulation of the
RT nuclear gene encoding the A subunit of chloroplast isozymes
RT glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana.";
RL Mol. Cell. Biol. 14:2525-2533 (1994).
DR EMBL; L14743; AAA31640.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
KW Chloroplast; Nuclear protein.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q31851 (1-12)

QY 9 GTGCCAAG 1
Db 8 ValProLys 10

RESULT 21
Q6JC67 PRELIMINARY; PRT; 12 AA.
ID Q6JC67;
AC Q6JC67;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Isoflavone synthase 2 (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15356384;
RA Subramanian S., Hu X., Lu G., Odell J.T., Yu O.;
RT "The promoters of two isoflavone synthase genes respond differentially
RT to modulation and defense signals in transgenic soybean roots.";
RL Plant Mol. Biol. 54:623-639 (2004).
DR EMBL; AY530097; AAT01228.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1298 MW; 5E7DE50411772DD7 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

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US-10-070-588A-112 (1-11) x Q6JC67 (1-12)
QY 3 TTGGCACTA 11
DB 5 LeuAlaLeu 7

RESULT 22
Q9UE87 PRELIMINARY; PRT; 13 AA.
AC Q9UE87;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Transforming growth factor alpha (Fragment).
GN Name:TFGA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89219018; PubMed=2907605;
RX Jakobovits E.B., Schlokot U., Vannice J.L., Derynck R., Levinson A.D.;
RT "The human transforming growth factor alpha promoter directs
RT transcription initiation from a single site in the absence of a TATA
RT sequence."
RL Mol. Cell. Biol. 8:5549-5554(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92168034; PubMed=1791840;
RA Saeki T., Cristiano A., Lynch M.J., Brattain M., Kim N., Normanno N.,
RA Kenney N., Ciardiello F., Salomon D.S.;
RT "Regulation by estrogen through the 5'-flanking region of the
RT transforming growth factor alpha gene."
RL Mol. Endocrinol. 5:1955-1963(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93364904; PubMed=8358733;
RA Lynch M.J., Pelosi L., Carbone J.M., Merwin J., Coleman K., Wang R.C.,
RA Lin P.P., Henry D.L., Brattain M.G.;
RT "Transforming growth factor-beta 1 induces transforming growth factor-
RT alpha promoter activity and transforming growth factor-alpha secretion
RT in the human colon adenocarcinoma cell line FET."
RL Cancer Res. 53:4041-4047(1993).
DR EMBL; M96868; AAA7958.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1318 MW; 2C6E4395FCBE36D8 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9UE87 (1-13)
QY 3 TTGGCACTA 11
DB 8 LeuAlaLeu 10

RESULT 23
Q6SE60 PRELIMINARY; PRT; 13 AA.
AC Q6SE60;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Idgf3 (Fragment).
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

US-10-070-588A-112 (1-11) x Q6JC67 (1-12)
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14762063; DOI=10.1101/gr.1329204;
RA Halligan D.L., Eyre-Walker A., Andolfatto P., Keightley P.D.;
RT "Patterns of evolutionary constraints in intronic and intergenic DNA
RT of Drosophila."
RL Genome Res. 14:273-279(2004).
DR EMBL; AY459538; AAR22997.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1392 MW; 220F3FF68C0CB733 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q6SE60 (1-13)
QY 3 TTGGCACTA 11
DB 9 LeuAlaLeu 11

RESULT 24
Q7RAS8 PRELIMINARY; PRT; 13 AA.
ID Q7RAS8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06421;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pette M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidlyum S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feidlyum T.V.,
RA Cho J.K., Quackenbush J., Sedegh M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002172; EAA18636.1; -.
KW Hypothetical protein.
SQ SEQUENCE 13 AA; 1500 MW; D06789FF2AEBCEB9 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7RAS8 (1-13)

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```
QY 3 TTGGCACTA 11
Db 2 LeuAlaLeu 4

RESULT 25
Q39380 PRELIMINARY; PRT; 13 AA.
ID Q39380;
AC Q39380;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IFA binding protein (sp10) (Fragment).
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Dok; TISSUE=Curd surface;
RA Willis G.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X97678; CAA66268.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1413 MW; DID4EA3926B42772 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q39380 (1-13)

QY 9 GTGCCAAG 1
Db 6 ValProlys 8

RESULT 26
Q6URV3 PRELIMINARY; PRT; 13 AA.
ID Q6URV3;
AC Q6URV3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE P-type R2R3 Myb protein (Fragment).
GN Name=Myb18;
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]_
RP SEQUENCE FROM N.A.
RC PubMed=14729259; DOI=10.1016/j.gene.2003.09.049;
RA Jiang C., Gu J., Chopra S., Gu X., Peterson T.;
RT "Ordered origin of the typical two- and three-repeat Myb genes.";
RL Gene 326:13-22(2004).
DR EMBL; AY363127; AAQ54841.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1504 MW; 240AF718A7B0C413 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
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US-10-070-588a-112 (1-11) x Q6URV3 (1-13)

QY 9 GTGCCAAG 1
Db 9 ValProlys 11

RESULT 27
Q62352 PRELIMINARY; PRT; 13 AA.
ID Q62352;
AC Q62352;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Trypsin precursor (Fragment).
GN Name=Prs83; Synonyms=Try3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=87066713; PubMed=3641189;
RA Stevenson B.J., Hagenbuechle O., Wellauer P.K.;
RT "Sequence organisation and transcriptional regulation of the mouse
RT elastase II and trypsin genes.";
RL Nucleic Acids Res. 14:8307-8330(1986).
DR EMBL; X04578; CAA28246.1; -.
DR MGD; MGI:102758; Prs83.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 13 Potential.
SQ SEQUENCE 13 AA; 1270 MW; 1EFFF43B6E14D720 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q62352 (1-13)

QY 3 TTGGCACTA 11
Db 7 LeuAlaLeu 9

RESULT 28
Q62354 PRELIMINARY; PRT; 13 AA.
ID Q62354;
AC Q62354;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Trypsin precursor (Fragment).
GN Name=Try4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=87066713; PubMed=3641189;
RA Stevenson B.J., Hagenbuechle O., Wellauer P.K.;
RT "Sequence organisation and transcriptional regulation of the mouse
RT elastase II and trypsin genes.";
RL Nucleic Acids Res. 14:8307-8330(1986).
DR EMBL; X04579; CAA28247.1; -.
DR MGD; MGI:102757; Try4.
KW Signal.
```

FT NON\_TER 1 1 Potential.  
FT SIGNAL <1 13  
SQ SEQUENCE 13 AA; 1320 MW; DDFFE2E16E14D729 CRC64;

Alignment Scores:  
Pred. No.: 4.57e+05 Length: 13  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q62354 (1-13)

QY 3 TTGGGCACTA 11  
Db 7 LeuAlaLeu 9

RESULT 29  
Q62355  
ID Q62355 PRELIMINARY; PRT; 13 AA.  
AC Q62355;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Trypsin precursor (Fragment).  
GN Name=Try4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/J;  
RX MEDLINE=87066713; PubMed=3641189;  
RA Stevenson B.J., Hagenbuechle O., Wellauer P.K.;  
RT "Sequence organisation and transcriptional regulation of the mouse  
elastase II and trypsin genes."  
RL Nucleic Acids Res. 14:8307-8330(1986).  
DR EMBL; X04580; CAA28248.1; --  
KW MGD; MGI:102757; Try4.  
DR Signal.  
KW NON\_TER 1 1  
FT SIGNAL <1 13 Potential.  
SQ SEQUENCE 13 AA; 1346 MW; DDFFF4200214D729 CRC64;

Alignment Scores:  
Pred. No.: 4.57e+05 Length: 13  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q62355 (1-13)

QY 3 TTGGGCACTA 11  
Db 7 LeuAlaLeu 9

RESULT 30  
Q9PWP4  
ID Q9PWP4 PRELIMINARY; PRT; 13 AA.  
AC Q9PWP4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Chimeric AFGP/trypsinogen-like serine protease precursor  
(Fragment).  
OS Disostichus mawsoni (Antarctic cod).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Perciformes;

OC Notothenioidae; Nototheniidae; Disostichus.  
OX NCBI\_TaxID=36200;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99447034; PubMed=10519545; DOI=10.1038/46721;  
RA Cheng C.H., Chen L.;  
RT "Evolution of an antifreeze glycoprotein.";  
RL Nature 401:443-444(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Cheng C.-H.C.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF134320; AAD37246.1; --  
DR GO; GO:0008233; F:peptidase activity; IEA.  
KW Protease; Signal.  
FT SIGNAL 1 >13 Potential.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1340 MW; 5186FA54AF1E2727 CRC64;

Alignment Scores:  
Pred. No.: 4.57e+05 Length: 13  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q9PWP4 (1-13)

QY 3 TTGGGCACTA 11  
Db 4 LeuAlaLeu 6

RESULT 31  
FERT\_TOBAC  
ID FERT\_TOBAC STANDARD; PRT; 14 AA.  
AC P82150;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Feruloyl-CoA thioesterase (EC 3.1.2.-) (Fragment).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OX lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE, CATALYTIC ACTIVITY, TISSUE SPECIFICITY, AND INDUCTION.  
RC STRAIN=cv. Samsum NN; TISSUE=Stem;  
RA Maury S., Geoffroy P., Legrand M.;  
RL Submitted (NOV-1999) to Swiss-Prot.  
CC -|- CATALYTIC ACTIVITY: Feruloyl-CoA + H(2)O = ferulate + CoA.  
CC -|- PATHWAY: Phenylpropanoid metabolism.  
CC -|- TISSUE SPECIFICITY: Expressed in stem, vascular tissues and  
tobacco mosaic virus infected leaves.  
CC -|- INDUCTION: By pathogen infection.  
KW Direct protein sequencing; Hydrolase.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1479 MW; 5F8B87AD9582AA7 CRC64;

Alignment Scores:  
Pred. No.: 4.47e+05 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-070-588a-112 (1-11) x FERT\_TOBAC (1-14)

QY 2 TTGGGCACT 10  
Db 10 PheGlyThr 12

RESULT 32					
ID	UC34_MAIZE	STANDARD;	PRT;	14 AA.	
AC	P80640;				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DE	03-JUL-2004	(Rel. 44, Last annotation update)			
DE	Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 360)				
DE	(Fragments).				
OS	Zea mays (Maize).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.				
ON	NCBI_TaxID=4577;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Coleoptile;				
RA	Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,				
RA	Pernollet J.-C., Zivy M., de Vienne D.;				
RT	"The maize two dimensional gel protein database: towards an integrated				
RL	genome analysis program."				
RL	Theor. Appl. Genet. 93:997-1005(1996).				
CC	-I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown				
CC	protein is: 5.7, its MW is: 41.1 kDa.				
CC	-I- CAUTION: The order of the peptides shown is uncertain.				
DR	Maize-2DPAGE; P80640; COLEOPTILE.				
DR	MaizeDB; 123965; -.				
KW	Direct protein sequencing.				
FT	NON_TER 1 1				
FT	NON_CONS 8 9				
FT	NON_TER 14 14				
EQ	SEQUENCE 14 AA; 1527 MW; DC525FF7B0BE682D CRC64;				
Alignment Scores:					
Pred. No.:	4.47e+05	Length:	14		
Score:	3.00	Matches:	3		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	1	Gaps:	0		
US-10-070-588A-112 (1-11) x UC34_MAIZE (1-14)					
Qy	3 TTGGCACTA 11				
Dd					
Dd	6 LeuAlaLeu 8				
RESULT 33					
ID	Q6JDV5	PRELIMINARY;	PRT;	14 AA.	
AC	Q6JDV5;				
DT	05-JUL-2004	(TEMBLrel. 27, Created)			
DT	05-JUL-2004	(TEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TEMBLrel. 27, Last annotation update)			
DE	Janus kinase 2 (Fragment).				
GN	Name=JAK2;				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
ON	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RK	PubMed=15174709; DOI=10.1111/j.1365-2052.2004.01128.x;				
RA	Wang H., Yu M., Liu B., Yerle M., Wang Y., Fan B., Zhu M.,				
RA	Li K.;				
RT	"Mapping of the porcine JAK2, JAK3 and TYK2 genes using somatic cell				
RT	and radiation hybrid panels";				
RL	Anim. Genet. 35:258-259(2004).				
DR	EMBL; AK509893; AAS79098.1; -.				
DR	GO; GO:001601; F.kinase activity; IEA.				
FT	NON_TER 1 1				

RA Gueneau de Novoa P., Williams K.P.;  
 RT "The tRNA website: reductive evolution of tRNA in plastids and other  
 endosymbionts.";  
 RL Nucleic Acids Res. 32:D104-D108(2004).  
 DR EMBL; AF550354; AAQ13670.1; --  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1490 MW; C5560BA69987A149 CRC64;

Alignment Scores:  
 Pred. No.: 4.47e+05 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q714T6 (1-14)

QY 3 TTGGGCAC 11  
 Db 11 LeuAlaLeu 13

RESULT 36

Q9MRV8 ID Q9MRV8 PRELIMINARY; PRT; 14 AA.  
 AC Q9MRV8;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE PSI 9 kDa protein (Fragment).  
 GN Name=psaC;  
 OS Aloe vera (Aloe) (Aloe barbadensis).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asphodelaceae;  
 OC Aloe.  
 OX NCBI\_TaxID=34199;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=21109831; PubMed=11181728;  
 RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;  
 RT "Primary transcripts of ndhD of Liliaceae and Aloaceae require editing  
 of the start and 20th codons.";  
 RL J. Exp. Bot. 52:179-180(2001).  
 DR EMBL; AJ278353; CAB96192.1; --  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Alignment Scores:  
 Pred. No.: 4.47e+05 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9MRV8 (1-14)

QY 1 CTTTGGCAC 9  
 Db 2 LeuTrpHis 4

RESULT 37

Q9MRV1 ID Q9MRV1 PRELIMINARY; PRT; 14 AA.  
 AC Q9MRV1;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE PSI 9 kDa protein (Fragment).

GN Name=psaC;  
 OS Allium sativum (Garlic).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
 OC Allium.  
 OX NCBI\_TaxID=4682;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=21109831; PubMed=11181728;  
 RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;  
 RT "Primary transcripts of ndhD of Liliaceae and Aloaceae require editing  
 of the start and 20th codons.";  
 RL J. Exp. Bot. 52:179-180(2001).  
 DR EMBL; AJ278351; CAB96187.1; --  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Alignment Scores:  
 Pred. No.: 4.47e+05 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9MRV1 (1-14)

QY 1 CTTTGGCAC 9  
 Db 2 LeuTrpHis 4

RESULT 38

Q9MRV4 ID Q9MRV4 PRELIMINARY; PRT; 14 AA.  
 AC Q9MRV4;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE PSI 9 kDa protein (Fragment).  
 GN Name=psaC;  
 OS Allium porrum (Leek).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
 OC Allium.  
 OX NCBI\_TaxID=4681;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=21109831; PubMed=11181728;  
 RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;  
 RT "Primary transcripts of ndhD of Liliaceae and Aloaceae require editing  
 of the start and 20th codons.";  
 RL J. Exp. Bot. 52:179-180(2001).  
 DR EMBL; AJ278352; CAB96185.1; --  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Alignment Scores:  
 Pred. No.: 4.47e+05 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9MRV4 (1-14)

```

SQ SEQUENCE 14 AA; 1544 MW; 811BBA1FD5040D1 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q64224 (1-14)
QY 2 TTTGGCACT 10
Db 8 PheGlyThr 10

RESULT 41
Q64225 PRELIMINARY; PRT; 14 AA.
AC Q64225;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE AtPB (Fragment).
GN Name=atpB;
OS Brachytheciastrum velutinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciaceae.
OX NCBI_TaxID=113273;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Velu1771;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciaceae, Bryopsida";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736269; AAU25911.1; -.
KW Chloroplast.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBA1FD5040D1 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q64225 (1-14)
QY 2 TTTGGCACT 10
Db 8 PheGlyThr 10

RESULT 42
Q64228 PRELIMINARY; PRT; 14 AA.
AC Q64228;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE AtPB (Fragment).
GN Name=atpB;
OS Brachytheciastrum trachypodium.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciaceae.
OX NCBI_TaxID=292612;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Trachypol1762, Trachypol1766, and Trachypol1770;

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QY 1 CTTGGCAC 9
Db 2 LeuTriPhis 4

RESULT 39
Q9NT61 PRELIMINARY; PRT; 14 AA.
AC Q9NT61;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSI 9 kDa protein (Fragment).
GN Name=psaC;
OS Allium cepa (Onion).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=4679;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=21109831; PubMed=11181728;
RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
RT "Primary transcripts of ndhD of Liliaceae and Aloaceae require editing
of the start and 20th codons.";
RL J. Exp. Bot. 52:179-180(2001).
DR EMBL; AJ278350; CAB96183.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03B7D911 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9NT61 (1-14)
QY 1 CTTGGCAC 9
Db 2 LeuTriPhis 4

RESULT 40
Q64224 PRELIMINARY; PRT; 14 AA.
AC Q64224;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE AtPB (Fragment).
GN Name=atpB;
OS Brachytheciastrum venustum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciaceae.
OX NCBI_TaxID=292614;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Venustum1704, and Venustum1705;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciaceae, Bryopsida";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736270; AAU25912.1; -.
DR EMBL; AY736271; AAU25913.1; -.
KW Chloroplast.
FT NON_TER 14

```



RA Vanderpoorten A.;  
RT "A molecular and morphological recircumscription of Brachytheciastrum  
TC (Brachytheciaceae, Bryopsida).";  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AV736266; AAU25908.1; -;  
DR EMBL; AV736267; AAU25909.1; -;  
DR EMBL; AV736268; AAU25910.1; -;  
KW Chloroplast.  
FT NON TER 14 14  
SQ SEQUENCE 14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;  
  
Alignment Scores:  
Pred. No.: 4.47e+05 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-070-588A-112 (1-11) x Q643A0 (1-14)  
QY 2 TTTGGCACT 10  
Db 8 PheGlyThr 10  
  
RESULT 43  
Q643A0 PRELIMINARY; PRT; 14 AA.  
AC Q643A0;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE AtpB (Fragment).  
GN Name=atpB;  
OS Brachytheciastrum collinum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.  
OX NCBI\_TaxID=219719;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Collinum1767, Collinum1769, and Collinum1765;  
RA Vanderpoorten A.;  
RT "A molecular and morphological recircumscription of Brachytheciastrum  
TC (Brachytheciaceae, Bryopsida).";  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AV736264; AAU25906.1; -;  
DR EMBL; AV736265; AAU25907.1; -;  
DR EMBL; AV736263; AAU25905.1; -;  
KW Chloroplast.  
FT NON TER 14 14  
SQ SEQUENCE 14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;  
  
Alignment Scores:  
Pred. No.: 4.47e+05 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-070-588A-112 (1-11) x Q643A0 (1-14)  
QY 2 TTTGGCACT 10  
Db 8 PheGlyThr 10  
  
RESULT 44  
Q7M1G6 PRELIMINARY; PRT; 14 AA.  
AC Q7M1G6;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Chaperone, TCPI-related.  
OS Avena sativa (Oat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Aveneae; Avena.  
OX NCBI\_TaxID=4498;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93288140; PubMed=8099715; DOI=10.1038/363644a0;  
RA Mummert E., Grimm R., Speth V., Eckerskorn C., Schiltz E.,  
RA Gatenby A.A., Schaefer E.;  
RT "A TCPI-related molecular chaperone from plants refolds phytochrome to  
its photoreversible form.";  
RL Nature 363:644-648(1993).  
DR PIR; S33802; S33802.  
SQ SEQUENCE 14 AA; 1525 MW; 439F33C92C4B6D77 CRC64;  
  
Alignment Scores:  
Pred. No.: 4.47e+05 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-070-588A-112 (1-11) x Q7M1G6 (1-14)  
QY 10 AGTGCCAAA 2  
Db 4 SerAlaLys 6  
  
RESULT 45  
Q7M1G7 PRELIMINARY; PRT; 14 AA.  
AC Q7M1G7;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Chaperone, TCPI-related.  
OS Avena sativa (Oat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Aveneae; Avena.  
OX NCBI\_TaxID=4498;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93288140; PubMed=8099715; DOI=10.1038/363644a0;  
RA Mummert E., Grimm R., Speth V., Eckerskorn C., Schiltz E.,  
RA Gatenby A.A., Schaefer E.;  
RT "A TCPI-related molecular chaperone from plants refolds phytochrome to  
its photoreversible form.";  
RL Nature 363:644-648(1993).  
DR PIR; S33801; S33801.  
SQ SEQUENCE 14 AA; 1607 MW; 438023C92C4B77C7 CRC64;  
  
Alignment Scores:  
Pred. No.: 4.47e+05 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-070-588A-112 (1-11) x Q7M1G7 (1-14)  
QY 10 AGTGCCAAA 2  
Db 4 SerAlaLys 6  
  
RESULT 46  
Q9FUX5 PRELIMINARY; PRT; 14 AA.  
ID Q9FUX5

```
AC Q9FUX5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 508 ribosomal protein L16 (Fragment)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Waxy (Fragment).
OS Symphoricarpos albus (Common snowberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Dipsacales; Caprifoliaceae; Symphoricarpos.
OX NCBI_TaxID=13702;
RN [1]
RP SEQUENCE FROM N.A.
RA Gould K.R., Donoghue M.J.;
RT "Phylogeny and biogeography of Triosteum (Caprifoliaceae).";
RL Harv. Pap. Bot. 5:157-166(2000).
DR EMBL; AF277633; AG331453.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1485 MW; DB8E206E5B7F8E5D CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9FUX5 (1-14)

QY 10 AGTGCCAAA 2
Db |||||
3 SerAlaLys 5

RESULT 47
Q8VU21 PRELIMINARY; PRT; 14 AA.
AC Q8VU21;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Oligopeptide transporter (Fragment).
GN Name=alia;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA Griffiths D.B., Hall L.M.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF246897; AAL68419.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1450 MW; 455351FA2F4BEE27 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q8VU21 (1-14)

QY 3 TTGGCACTA 11
Db |||||
8 LeuAlaLeu 10

RESULT 48
Q711Z6 PRELIMINARY; PRT; 14 AA.
ID Q711Z6
AC Q711Z6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

AC Q9FUX5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 508 ribosomal protein L16 (Fragment)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Waxy (Fragment).
OS Symphoricarpos albus (Common snowberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Dipsacales; Caprifoliaceae; Symphoricarpos.
OX NCBI_TaxID=13702;
RN [1]
RP SEQUENCE FROM N.A.
RA Gould K.R., Donoghue M.J.;
RT "Phylogeny and biogeography of Triosteum (Caprifoliaceae).";
RL Harv. Pap. Bot. 5:157-166(2000).
DR EMBL; AF277633; AG331453.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1485 MW; DB8E206E5B7F8E5D CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q711Z6 (1-14)

QY 9 GTGCCAAAG 1
Db |||||
4 ValProLys 6

RESULT 49
Q9UR64 PRELIMINARY; PRT; 15 AA.
ID Q9UR64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 46 kDa heme-containing ascorbate oxidase (Fragment).
OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=5322;
RN [1]
RP SEQUENCE.
RX MEDLINE=96216386; PubMed=8621708; DOI=10.1074/jbc.271.36.22052;
RA Kim Y.R., Yu S.W., Lee S.R., Hwang Y.Y., Kang S.O.;
RT "A heme-containing ascorbate oxidase from Pleurotus ostreatus.";
RL J. Biol. Chem. 271:3105-3111(1996).
SQ SEQUENCE 15 AA; 1738 MW; FF939C118BD30D75 CRC64;

Alignment Scores:
Pred. No.: 4.38e+05 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9UR64 (1-15)

QY 3 TTGGCACTA 11
Db |||||
11 LeuAlaLeu 13

RESULT 50
Q9WZR5 PRELIMINARY; PRT; 15 AA.
ID Q9WZR5;
AC Q9WZR5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
```

DE Interleukin 4 variant IL-4int2A (Fragment).  
GN Name=IL-4;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=20304414; PubMed=10843729; DOI=10.1006/cyto.1999.0658;  
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;  
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the  
RT European rabbit (Oryctolagus cuniculus).";  
RL Cytokine 12:555-565(2000).  
DR EMBL; AF169172; AAF86656.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 15 AA; 1586 MW; 876C550E85307B55 CRC64;

Alignment Scores:  
Pred. No.: 4.38e+05 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9MZR5 (1-15)

QY 9 GTGCCAAG 1  
Db 12 ValProLys 14

Search completed: March 12, 2005, 11:07:34  
Job time : 61.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 10:59:19 ; Search time 17 Seconds  
(without alignments)  
96.605 Million cell updates/sec

Title: US-10-070-588a-112

Perfect score: 3

Sequence: 1 ctttgcacta 11

Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Word size: 1

Total number of hits satisfying chosen parameters: 895877

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US10070588/runat\_10032005\_120706\_15259/app\_query.fasta.1.199  
-DB=issued Patents AA -QMT=fastan -SUFFIX=olin2p.ra1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=500 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=1 -MAXLEN=200000000  
-USER=US10070588 -CGEN 1 1 30 @runat\_10032005\_120706\_15259 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGESQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	3	100.0	8	1	US-07-752-101A-4
2	3	100.0	8	1	US-08-204-656B-13
3	3	100.0	8	1	US-08-079-741A-101
4	3	100.0	8	1	US-07-939-065A-101
5	3	100.0	8	1	US-08-470-702-13
6	3	100.0	8	1	US-08-467-831-13
7	3	100.0	8	1	US-08-331-657-3
8	3	100.0	8	1	US-08-571-985-16
C 8	3	100.0	8	1	US-08-408-604A-181
C 9	3	100.0	8	1	US-08-408-604A-207
11	3	100.0	8	1	US-08-633-760-3
12	3	100.0	8	2	US-08-668-871-9
C 1	3	100.0	8	1	US-07-752-101A-4
2	3	100.0	8	1	US-08-204-656B-13
3	3	100.0	8	1	US-08-079-741A-101
4	3	100.0	8	1	US-07-939-065A-101
5	3	100.0	8	1	US-08-470-702-13
6	3	100.0	8	1	US-08-467-831-13
7	3	100.0	8	1	US-08-331-657-3
8	3	100.0	8	1	US-08-571-985-16
C 8	3	100.0	8	1	US-08-408-604A-181
C 9	3	100.0	8	1	US-08-408-604A-207
11	3	100.0	8	1	US-08-633-760-3
12	3	100.0	8	2	US-08-668-871-9

Sequence 9, Appli	8	2	US-08-669-683-9	100.0	3	13
Sequence 51, Appli	8	2	US-08-482-651-51	100.0	3	14
Sequence 163, App	8	2	US-08-968-676-163	100.0	C	15
Sequence 53, Appli	8	2	US-09-016-366A-53	100.0	3	16
Sequence 16, Appli	8	2	US-09-116-766-16	100.0	C	17
Sequence 123, App	8	2	US-08-310-912A-123	100.0	3	18
Sequence 125, App	8	2	US-08-310-912A-125	100.0	3	19
Sequence 366, App	8	2	US-08-444-818-366	100.0	3	20
Sequence 367, App	8	3	US-08-444-818-367	100.0	3	21
Sequence 368, App	8	3	US-08-444-818-368	100.0	3	22
Sequence 369, App	8	3	US-08-444-818-369	100.0	3	23
Sequence 387, App	8	3	US-08-444-818-387	100.0	3	24
Sequence 14, Appli	8	3	US-09-296-284-14	100.0	C	25
Sequence 54, Appli	8	3	US-08-660-092-54	100.0	3	26
Sequence 188, App	8	3	US-08-660-092-188	100.0	3	27
Sequence 123, App	8	3	US-09-301-085-123	100.0	3	28
Sequence 125, App	8	3	US-09-301-085-125	100.0	3	29
Sequence 19, Appli	8	3	US-09-394-630-19	100.0	C	30
Sequence 54, Appli	8	4	US-09-160-513-54	100.0	3	31
Sequence 188, App	8	4	US-09-160-513-188	100.0	3	32
Sequence 22, Appli	8	4	US-09-675-922-22	100.0	3	33
Sequence 15, Appli	8	4	US-09-704-251-15	100.0	3	34
Sequence 124, App	8	4	US-08-635-886C-124	100.0	3	35
Sequence 125, App	8	4	US-08-635-886C-125	100.0	3	36
Sequence 8, Appli	8	4	US-08-964-747-8	100.0	3	37
Sequence 12, Appli	8	4	US-09-562-913-8	100.0	3	38
Sequence 124, App	8	4	US-09-269-439-12	100.0	3	39
Sequence 125, App	8	4	US-08-974-690C-124	100.0	3	40
Sequence 125, App	8	4	US-08-974-690C-125	100.0	3	41
Sequence 186, App	8	4	US-09-721-108-186	100.0	3	42
Sequence 124, App	8	4	US-08-974-685-124	100.0	3	43
Sequence 125, App	8	4	US-08-974-685-125	100.0	3	44
Sequence 10, Appli	8	4	US-09-707-263A-10	100.0	3	45
Sequence 17, Appli	8	4	US-09-707-263A-17	100.0	C	46
Sequence 4, Appli	8	4	US-09-403-269-4	100.0	C	47
Sequence 163, App	8	4	US-09-261-894A-163	100.0	C	48
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Sequence 125, App	8	5	PCT-US95-04589-125	100.0	3	50
Sequence 20, Appli	8	9	US-07-862-831A-20	100.0	C	51
Sequence 20, Appli	8	9	US-08-126-564A-20	100.0	C	52
Sequence 14, Appli	8	9	US-07-994-133-14	100.0	C	53
Sequence 9, Appli	8	9	US-08-003-311B-9	100.0	3	54
Sequence 8, Appli	8	9	US-08-350-884-8	100.0	3	55
Sequence 11, Appli	8	9	US-08-350-884-11	100.0	3	56
Sequence 14, Appli	8	9	US-08-261-432-9	100.0	3	57
Sequence 9, Appli	8	9	US-08-196-630A-10	100.0	3	58
Sequence 10, Appli	8	9	US-08-454-207A-7	100.0	3	59
Sequence 7, Appli	8	9	US-08-454-207A-8	100.0	3	60
Sequence 9, Appli	8	9	US-08-454-207A-9	100.0	3	61
Sequence 10, Appli	8	9	US-08-454-207A-10	100.0	3	62
Sequence 12, Appli	8	9	US-08-454-207A-12	100.0	3	63
Sequence 13, Appli	8	9	US-08-454-207A-13	100.0	3	64
Sequence 14, Appli	8	9	US-08-454-207A-14	100.0	3	65
Sequence 15, Appli	8	9	US-08-454-207A-15	100.0	3	66
Sequence 16, Appli	8	9	US-08-454-207A-16	100.0	3	67
Sequence 17, Appli	8	9	US-08-454-207A-17	100.0	3	68
Sequence 18, Appli	8	9	US-08-454-207A-18	100.0	3	69
Sequence 19, Appli	8	9	US-08-454-207A-19	100.0	3	70
Sequence 20, Appli	8	9	US-08-454-207A-20	100.0	3	71
Sequence 21, Appli	8	9	US-08-454-207A-21	100.0	3	72
Sequence 22, Appli	8	9	US-08-454-207A-22	100.0	3	73
Sequence 29, Appli	8	9	US-08-454-207A-29	100.0	3	74
Sequence 30, Appli	8	9	US-08-454-207A-30	100.0	3	75
Sequence 31, Appli	8	9	US-08-454-207A-31	100.0	3	76
Sequence 32, Appli	8	9	US-08-454-207A-32	100.0	3	77
Sequence 33, Appli	8	9	US-08-454-207A-33	100.0	3	78
Sequence 34, Appli	8	9	US-08-454-207A-34	100.0	3	79
Sequence 35, Appli	8	9	US-08-454-207A-35	100.0	3	80
Sequence 36, Appli	8	9	US-08-454-207A-36	100.0	3	81
Sequence 37, Appli	8	9	US-08-454-207A-37	100.0	3	82
Sequence 38, Appli	8	9	US-08-454-207A-38	100.0	3	83
Sequence 39, Appli	8	9	US-08-454-207A-39	100.0	3	84
Sequence 39, Appli	8	9	US-08-454-207A-39	100.0	3	85

86	3	100.0	9	1	US-08-454-207A-40	Sequence 40, Appl	159	3	100.0	9	3	US-09-518-046-60	Sequence 60, Appl
87	3	100.0	9	1	US-08-454-207A-41	Sequence 41, Appl	160	3	100.0	9	3	US-09-567-995-9	Sequence 9, Appl
88	3	100.0	9	1	US-08-454-207A-48	Sequence 48, Appl	161	3	100.0	9	3	US-09-406-781-19	Sequence 19, Appl
89	3	100.0	9	1	US-08-454-207A-49	Sequence 49, Appl	162	3	100.0	9	3	US-09-492-543-33	Sequence 33, Appl
90	3	100.0	9	1	US-08-454-207A-50	Sequence 50, Appl	163	3	100.0	9	3	US-09-492-543-53	Sequence 53, Appl
91	3	100.0	9	1	US-08-454-207A-51	Sequence 51, Appl	164	3	100.0	9	3	US-09-492-543-86	Sequence 86, Appl
92	3	100.0	9	1	US-08-454-207A-52	Sequence 52, Appl	165	3	100.0	9	3	US-09-492-543-96	Sequence 96, Appl
93	3	100.0	9	1	US-08-454-207A-53	Sequence 53, Appl	166	3	100.0	9	3	US-09-492-543-106	Sequence 106, App
94	3	100.0	9	1	US-08-454-207A-54	Sequence 54, Appl	167	3	100.0	9	3	US-09-492-543-111	Sequence 111, App
95	3	100.0	9	1	US-08-454-207A-57	Sequence 57, Appl	168	3	100.0	9	3	US-09-492-543-123	Sequence 123, App
96	3	100.0	9	1	US-08-454-207A-58	Sequence 58, Appl	169	3	100.0	9	3	US-09-492-543-138	Sequence 138, App
97	3	100.0	9	1	US-08-454-207A-59	Sequence 59, Appl	170	3	100.0	9	3	US-09-492-543-142	Sequence 142, App
98	3	100.0	9	1	US-08-454-207A-60	Sequence 60, Appl	171	3	100.0	9	3	US-09-241-268-1	Sequence 1, Appl
99	3	100.0	9	1	US-08-454-207A-61	Sequence 61, Appl	172	3	100.0	9	3	US-08-292-492D-5	Sequence 5, Appl
100	3	100.0	9	1	US-08-454-207A-62	Sequence 62, Appl	173	3	100.0	9	3	US-09-705-160-39	Sequence 39, Appl
101	3	100.0	9	1	US-08-454-207A-63	Sequence 63, Appl	174	3	100.0	9	3	US-09-256-194-14	Sequence 14, Appl
102	3	100.0	9	1	US-08-454-207A-64	Sequence 64, Appl	175	3	100.0	9	4	US-09-165-863-6	Sequence 6, Appl
103	3	100.0	9	1	US-08-454-207A-65	Sequence 65, Appl	176	3	100.0	9	4	US-09-160-513-13	Sequence 13, Appl
104	3	100.0	9	1	US-08-454-207A-66	Sequence 66, Appl	177	3	100.0	9	4	US-09-160-513-40	Sequence 40, Appl
105	3	100.0	9	1	US-08-454-207A-67	Sequence 67, Appl	178	3	100.0	9	4	US-09-697-884-50	Sequence 50, Appl
106	3	100.0	9	1	US-08-454-207A-68	Sequence 68, Appl	179	3	100.0	9	4	US-09-495-562-1	Sequence 1, Appl
107	3	100.0	9	1	US-08-454-207A-69	Sequence 69, Appl	180	3	100.0	9	4	US-09-435-524-3	Sequence 3, Appl
108	3	100.0	9	1	US-08-454-207A-70	Sequence 70, Appl	181	3	100.0	9	4	US-09-435-524-4	Sequence 4, Appl
109	3	100.0	9	1	US-08-709-173-8	Sequence 8, Appl	182	3	100.0	9	4	US-09-847-185-25	Sequence 25, Appl
110	3	100.0	9	1	US-08-709-173-11	Sequence 11, Appl	183	3	100.0	9	4	US-09-213-383-19	Sequence 19, Appl
111	3	100.0	9	1	US-08-709-173-14	Sequence 14, Appl	184	3	100.0	9	4	US-08-403-459-49	Sequence 49, Appl
112	3	100.0	9	1	US-08-638-911A-15	Sequence 15, Appl	185	3	100.0	9	4	US-08-403-459-50	Sequence 50, Appl
113	3	100.0	9	1	US-08-638-911A-18	Sequence 18, Appl	186	3	100.0	9	4	US-09-289-350-6	Sequence 6, Appl
114	3	100.0	9	1	US-08-638-911A-21	Sequence 21, Appl	187	3	100.0	9	4	US-09-574-749B-8	Sequence 8, Appl
115	3	100.0	9	1	US-08-363-691-3	Sequence 3, Appl	188	3	100.0	9	4	US-09-341-982-92	Sequence 92, Appl
116	3	100.0	9	1	US-08-787-547-7	Sequence 7, Appl	189	3	100.0	9	4	US-09-880-132-19	Sequence 19, Appl
117	3	100.0	9	2	US-08-468-819-19	Sequence 19, Appl	190	3	100.0	9	4	US-09-318-141-6	Sequence 6, Appl
118	3	100.0	9	2	US-08-482-651-10	Sequence 10, Appl	191	3	100.0	9	4	US-09-318-243-38	Sequence 38, Appl
119	3	100.0	9	2	US-08-482-651-37	Sequence 37, Appl	192	3	100.0	9	4	US-09-918-243-43	Sequence 43, Appl
120	3	100.0	9	2	US-08-389-360-3	Sequence 3, Appl	193	3	100.0	9	4	US-09-918-243-46	Sequence 46, Appl
121	3	100.0	9	2	US-08-389-360-4	Sequence 4, Appl	194	3	100.0	9	4	US-09-604-958-8	Sequence 8, Appl
122	3	100.0	9	2	US-08-709-177-8	Sequence 8, Appl	195	3	100.0	9	4	US-09-382-497-3	Sequence 3, Appl
123	3	100.0	9	2	US-08-709-177-11	Sequence 11, Appl	196	3	100.0	9	4	US-09-382-497-4	Sequence 4, Appl
124	3	100.0	9	2	US-08-902-516-25	Sequence 25, Appl	197	3	100.0	9	4	US-09-750-876-6	Sequence 6, Appl
125	3	100.0	9	2	US-08-968-676-13	Sequence 13, Appl	198	3	100.0	9	4	US-09-750-876-7	Sequence 7, Appl
126	3	100.0	9	2	US-08-968-676-49	Sequence 49, Appl	199	3	100.0	9	4	US-09-750-876-8	Sequence 8, Appl
127	3	100.0	9	2	US-08-993-738A-1	Sequence 1, Appl	200	3	100.0	9	4	US-09-454-204A-10	Sequence 10, Appl
128	3	100.0	9	2	US-09-036-582-6	Sequence 6, Appl	201	3	100.0	9	4	US-09-721-108-185	Sequence 185, App
129	3	100.0	9	2	US-08-318-856A-5	Sequence 5, Appl	202	3	100.0	9	4	US-09-169-717B-12	Sequence 12, Appl
130	3	100.0	9	2	US-08-318-856A-53	Sequence 53, Appl	203	3	100.0	9	4	US-09-647-372B-8	Sequence 8, Appl
131	3	100.0	9	2	US-08-986-234-65	Sequence 65, Appl	204	3	100.0	9	4	US-09-647-372B-10	Sequence 10, Appl
132	3	100.0	9	2	US-08-986-234-66	Sequence 66, Appl	205	3	100.0	9	4	US-09-633-994-5	Sequence 5, Appl
133	3	100.0	9	2	US-08-986-234-99	Sequence 99, Appl	206	3	100.0	9	4	US-09-806-769-6	Sequence 6, Appl
134	3	100.0	9	2	US-08-986-234-100	Sequence 100, App	207	3	100.0	9	4	US-09-396-315-50	Sequence 50, Appl
135	3	100.0	9	2	US-08-159-339A-182	Sequence 182, App	208	3	100.0	9	4	US-09-462-453-2	Sequence 2, Appl
136	3	100.0	9	3	US-08-159-339A-769	Sequence 769, App	209	3	100.0	9	4	US-09-995-587A-8	Sequence 8, Appl
137	3	100.0	9	3	US-08-159-339A-1008	Sequence 1008, Ap	210	3	100.0	9	4	US-09-171-553B-15	Sequence 15, Appl
138	3	100.0	9	3	US-08-159-339A-1009	Sequence 1009, Ap	211	3	100.0	9	4	US-09-124-398-15	Sequence 15, Appl
139	3	100.0	9	3	US-08-159-339A-1010	Sequence 1010, Ap	212	3	100.0	9	4	US-09-408-036B-38	Sequence 38, Appl
140	3	100.0	9	3	US-09-038-328-3	Sequence 3, Appl	213	3	100.0	9	4	US-09-631-863A-95	Sequence 95, Appl
141	3	100.0	9	3	US-09-038-328-4	Sequence 4, Appl	214	3	100.0	9	4	US-09-261-894A-13	Sequence 13, Appl
142	3	100.0	9	3	US-08-551-510-6	Sequence 6, Appl	215	3	100.0	9	4	US-09-261-894A-49	Sequence 49, Appl
143	3	100.0	9	3	US-08-551-510-7	Sequence 7, Appl	216	3	100.0	9	4	US-09-693-746-118	Sequence 118, App
144	3	100.0	9	3	US-08-551-510-8	Sequence 8, Appl	217	3	100.0	9	4	US-09-980-177A-1	Sequence 1, Appl
145	3	100.0	9	3	US-08-660-092-13	Sequence 13, Appl	218	3	100.0	9	4	PCT-US94-09143-20	Sequence 20, Appl
146	3	100.0	9	3	US-08-660-092-40	Sequence 40, Appl	219	3	100.0	9	5	PCT-US94-09143-36	Sequence 36, Appl
147	3	100.0	9	3	US-09-183-931-39	Sequence 39, Appl	220	3	100.0	9	5	PCT-US95-04121-36	Sequence 41, Appl
148	3	100.0	9	3	US-08-551-510-6	Sequence 6, Appl	221	3	100.0	10	1	US-08-164-839-41	Sequence 41, Appl
149	3	100.0	9	3	US-08-551-510-7	Sequence 7, Appl	222	3	100.0	10	1	US-08-371-930-11	Sequence 11, Appl
150	3	100.0	9	3	US-08-551-510-8	Sequence 8, Appl	223	3	100.0	10	1	US-08-462-949-23	Sequence 23, Appl
151	3	100.0	9	3	US-09-183-906-9	Sequence 9, Appl	224	3	100.0	10	1	US-08-583-799-41	Sequence 41, Appl
152	3	100.0	9	3	US-09-171-878-14	Sequence 14, Appl	225	3	100.0	10	1	US-08-239-854-7	Sequence 7, Appl
153	3	100.0	9	3	US-08-713-354C-1	Sequence 1, Appl	226	3	100.0	10	1	US-08-330-163-45	Sequence 45, Appl
154	3	100.0	9	3	US-09-166-448-50	Sequence 50, Appl	227	3	100.0	10	1	US-08-023-764B-23	Sequence 23, Appl
155	3	100.0	9	3	US-09-502-600-38	Sequence 38, Appl	228	3	100.0	10	1	US-08-214-650-2	Sequence 2, Appl
156	3	100.0	9	3	US-09-502-600-43	Sequence 43, Appl	229	3	100.0	10	1	US-08-454-207A-2	Sequence 2, Appl
157	3	100.0	9	3	US-09-502-600-46	Sequence 46, Appl	230	3	100.0	10	1	US-08-454-207A-5	Sequence 5, Appl
158	3	100.0	9	3	US-09-518-046-48	Sequence 48, Appl	231	3	100.0	10	1	US-08-482-111-45	Sequence 45, Appl

232	3	100.0	10	2	US-08-482-651-59	Sequence 59, Appl	c 305	3	100.0	10	4	US-09-261-894A-16	Sequence 16, Appl
c 233	3	100.0	10	2	US-08-685-589A-132	Sequence 132, App	c 306	3	100.0	10	4	US-09-261-894A-17	Sequence 17, Appl
c 234	3	100.0	10	2	US-08-968-676-16	Sequence 16, Appl	c 307	3	100.0	10	4	US-09-261-894A-45	Sequence 45, Appl
c 235	3	100.0	10	2	US-08-968-676-17	Sequence 17, Appl	c 308	3	100.0	10	4	US-09-261-894A-47	Sequence 47, Appl
c 236	3	100.0	10	2	US-08-968-676-45	Sequence 45, Appl	c 309	3	100.0	10	4	US-09-261-894A-50	Sequence 50, Appl
c 237	3	100.0	10	2	US-08-968-676-47	Sequence 47, Appl	c 310	3	100.0	10	4	US-09-261-894A-51	Sequence 51, Appl
c 238	3	100.0	10	2	US-08-968-676-50	Sequence 50, Appl	c 311	3	100.0	10	4	US-09-261-894A-52	Sequence 52, Appl
c 239	3	100.0	10	2	US-08-968-676-51	Sequence 51, Appl	c 312	3	100.0	10	4	US-09-261-894A-53	Sequence 53, Appl
c 240	3	100.0	10	2	US-08-968-676-52	Sequence 52, Appl	c 313	3	100.0	10	4	US-09-261-894A-54	Sequence 54, Appl
c 241	3	100.0	10	2	US-08-968-676-53	Sequence 53, Appl	c 314	3	100.0	10	4	US-09-261-894A-55	Sequence 55, Appl
c 242	3	100.0	10	2	US-08-968-676-54	Sequence 54, Appl	c 315	3	100.0	10	4	US-09-261-894A-56	Sequence 56, Appl
c 243	3	100.0	10	2	US-08-968-676-55	Sequence 55, Appl	c 316	3	100.0	10	4	US-09-261-894A-57	Sequence 57, Appl
c 244	3	100.0	10	2	US-08-968-676-56	Sequence 56, Appl	c 317	3	100.0	10	4	US-09-261-894A-58	Sequence 58, Appl
c 245	3	100.0	10	2	US-08-968-676-57	Sequence 57, Appl	c 318	3	100.0	10	4	US-09-261-894A-94	Sequence 94, Appl
c 246	3	100.0	10	2	US-08-968-676-58	Sequence 58, Appl	c 319	3	100.0	10	4	US-09-261-894A-107	Sequence 107, App
c 247	3	100.0	10	2	US-08-968-676-94	Sequence 94, Appl	c 320	3	100.0	10	4	US-09-261-894A-108	Sequence 108, App
c 248	3	100.0	10	2	US-08-968-676-107	Sequence 107, App	c 321	3	100.0	10	4	US-09-261-894A-109	Sequence 109, App
c 249	3	100.0	10	2	US-08-968-676-108	Sequence 108, App	c 322	3	100.0	10	4	US-09-261-894A-110	Sequence 110, App
c 250	3	100.0	10	2	US-08-968-676-109	Sequence 109, App	c 323	3	100.0	10	4	US-09-261-894A-111	Sequence 111, App
c 251	3	100.0	10	2	US-08-968-676-110	Sequence 110, App	c 324	3	100.0	10	4	US-09-261-894A-112	Sequence 112, App
c 252	3	100.0	10	2	US-08-968-676-111	Sequence 111, App	c 325	3	100.0	10	4	US-09-261-894A-113	Sequence 113, App
c 253	3	100.0	10	2	US-08-968-676-112	Sequence 112, App	c 326	3	100.0	10	4	US-09-693-746-55	Sequence 55, Appl
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c 258	3	100.0	10	3	US-08-822-586-2	Sequence 2, Appl	c 331	3	100.0	10	5	PCT-US95-02121-126	Sequence 126, App
c 259	3	100.0	10	3	US-08-822-586-6	Sequence 6, Appl	c 332	3	100.0	10	5	PCT-US95-02121-133	Sequence 133, App
c 260	3	100.0	10	3	US-08-822-586-10	Sequence 10, Appl	c 333	3	100.0	10	5	PCT-US95-06157-14	Sequence 14, Appl
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c 263	3	100.0	10	3	US-08-822-586-38	Sequence 38, Appl	c 336	3	100.0	11	1	US-08-347-198A-5	Sequence 5, Appl
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c 286	3	100.0	10	4	US-09-106-568E-26	Sequence 26, Appl	c 359	3	100.0	11	4	US-09-538-873-9	Sequence 9, Appl
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c 303	3	100.0	10	4	US-10-062-848-62	Sequence 62, Appl	c 376	3	100.0	11	5	PCT-US94-07644A-12	Sequence 12, Appl
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385	3	100.0	12	1	US-08-378-761A-56	Sequence 56, Appl	458	3	100.0	13	1	US-08-390-156A-106	Sequence 106, App
386	3	100.0	12	1	US-08-129-456A-17	Sequence 17, Appl	459	3	100.0	13	1	US-08-200-900A-24	Sequence 24, Appl
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c 393	3	100.0	12	2	US-08-540-412-79	Sequence 79, Appl	466	3	100.0	13	2	US-08-632-514C-21	Sequence 21, Appl
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c 395	3	100.0	12	2	US-07-737-371E-76	Sequence 76, Appl	c 468	3	100.0	13	2	US-08-455-968E-12	Sequence 12, Appl
c 396	3	100.0	12	2	US-08-968-676-15	Sequence 15, Appl	c 469	3	100.0	13	2	US-08-968-676-11	Sequence 11, Appl
c 397	3	100.0	12	2	US-08-968-676-29	Sequence 29, Appl	c 470	3	100.0	13	2	US-08-968-676-30	Sequence 30, Appl
c 398	3	100.0	12	2	US-08-450-497-23	Sequence 23, Appl	471	3	100.0	13	2	US-08-433-133-24	Sequence 24, Appl
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Sequence 79, Appl

Patent No. 5248606

Patent No. 5248606

Sequence 5, Appl

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Sequence 9, Appl

Sequence 12, Appl

Sequence 26, Appl

Sequence 473, App

Sequence 96, Appl

Sequence 9, Appl

Sequence 10, App

Sequence 181, App

Sequence 2, Appl

US-09-693-746-74

PCT-US95-08156-79

5248606-38

5248606-38

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US-09-721-870-96

US-10-067-443-9

US-09-155-165-10

US-09-721-108-181

US-09-749-233-2

ALIGNMENTS

RESULT 1

US-07-752-101A-4

Sequence 4, Application US/07752101A

Patent No. 5326857

GENERAL INFORMATION:

APPLICANT: Yamamoto, Fumi-ichiro

APPLICANT: White, Thayer

APPLICANT: Hakomori, Sen-itiroh

APPLICANT: Clausen, Henrik

TITLE OF INVENTION: ABO GENOTYPING

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

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CITY: Seattle

STATE: Washington

COUNTRY: U.S.

ZIP: 98104

COMPUTER READABLE FORM:

## ALIGNMENTS

## RESULT 1

US-07-752-101A-4  
; Sequence 4, Application US/07752101A  
; Patent No. 5326857  
; GENERAL INFORMATION:  
; APPLICANT: Yamamoto, Fumi-ichiro  
; APPLICANT: White, Thayer  
; APPLICANT: Hakomori, Sen-itiroh  
; APPLICANT: Clausen, Henrik  
; TITLE OF INVENTION: ABO GENOTYPING  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.  
; ZIP: 98104  
; COMPUTER READABLE FORM:



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/752.101A  
FILING DATE: 19910829  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 150036.406C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-07-752-101A-4

Alignment Scores:  
Pred. No.: 1.85e+07  
Score: 3.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 1  
Gaps: 0

US-10-070-588A-112 (1-11) x US-07-752-101A-4 (1-8)

Qy 9 GTGCCAAG 1  
Db 6 ValProlys 8

RESULT 2  
US-08-204-656B-13  
Sequence 13, Application US/08204656B  
Patent No. 5538882  
GENERAL INFORMATION:  
APPLICANT: Matsui, Ikuo  
APPLICANT: Ishikawa, Kazuhiko  
APPLICANT: Miyairi, Sachio  
APPLICANT: Honda, Koichi  
TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,  
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing  
TITLE OF INVENTION: Oligosaccharide Using The Enzyme  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
STREET: 8110 Gatehouse Road, Suite 500 East  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22042  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204.656B  
FILING DATE: 02-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiner, Marc S.

REGISTRATION NUMBER: 32,181  
REFERENCE/DOCKET NUMBER: 234-252P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-204-656B-13

Alignment Scores:  
Pred. No.: 1.85e+07  
Score: 3.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 1  
Gaps: 0

US-10-070-588A-112 (1-11) x US-08-204-656B-13 (1-8)

Qy 2 TTTGGCACT 10  
Db 3 PheGlyThr 5

RESULT 3  
US-08-079-741A-101  
Sequence 101, Application US/08079741A  
Patent No. 5585275  
GENERAL INFORMATION:  
APPLICANT: SURNAME, OTHER NAMES and/or INITIALS  
APPLICANT: Johnson, Charles R.  
APPLICANT: Giebel, Lutz B.  
TITLE OF INVENTION: Pilot Apparatus For Peptide  
TITLE OF INVENTION: Synthesis and Screening  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS: Inventors'/Assignee's Counsel  
ADDRESSEE: ROSENBLUM, PARISH & ISAACS  
STREET: 160 W. Santa Clara Street, Suite 1500  
CITY: San Jose  
STATE: California  
COUNTRY: USA  
ZIP: 95113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3-1/2 inch, 1.44M byte  
MEDIUM TYPE: storage  
COMPUTER: IBM Clone  
OPERATING SYSTEM: MS-DOS 5.00  
SOFTWARE: WordPerfect 5.1, ASCII format (DOS text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/079.741A  
FILING DATE: 18-June-1993  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/939,065  
FILING DATE: 02-Sept-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: DULIN, JACQUES M.  
REGISTRATION NUMBER: 24,067  
REFERENCE/DOCKET NUMBER: 5303-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 977-0120  
TELEFAX: (408) 977-0129  
INFORMATION FOR SEQ ID NO: 101:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8

```

; TYPE: Amino Acids
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION:
; NAME/KEY: Pepsyn-K Bead Test Peptide
; LOCATION:
; IDENTIFICATION METHOD: Constructed using a
; IDENTIFICATION METHOD: Milligen/Biossearch Model 9600 peptide synthesizer.
; OTHER INFORMATION: Biological activity not
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 101: From 1 to 8
;
US-08-079-741A-101
Alignment Scores:
Pred No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-079-741A-101 (1-8)
Qy 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 4
US-07-939-065A-101
; Sequence 101, Application US/07939065A
; Patent No. 5591646
; GENERAL INFORMATION:
; APPLICANT: SURNAME, OTHER NAMES and/or INITIALS
; APPLICANT: Johnson, Charles R.
; APPLICANT: Giebel, Lutz B.
; TITLE OF INVENTION: Method and Apparatus For Peptide
; TITLE OF INVENTION: Synthesis and Screening
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS: Inventors'/Assignee's Counsel
; ADDRESSEE: PILLSBURY MADISON & SUTRO
; STREET: Ten Almaden Boulevard, Suite 800
; CITY: San Jose
; STATE: California
; COUNTRY: USA
; ZIP: 95113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3-1/2 inch, 1.44M byte
; MEDIUM TYPE: storage
; COMPUTER: IBM Clone
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: Wordperfect 5.2, ASCII format (DOS text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/939,065A
; FILING DATE: 02-Sept-1992
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NA
; FILING DATE: NA
; ATTORNEY/AGENT INFORMATION:
; NAME: DULIN, JACQUES M.
; REGISTRATION NUMBER: 24,067

; TYPE: Amino Acids
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION:
; NAME/KEY: Pepsyn-K Bead Test Peptide
; LOCATION:
; IDENTIFICATION METHOD: Constructed using a
; IDENTIFICATION METHOD: Milligen/Biossearch Model 9600 peptide synthesizer.
; OTHER INFORMATION: Biological activity not
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 101: From 1 to 8
;
US-07-939-065A-101
Alignment Scores:
Pred No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-07-939-065A-101 (1-8)
Qy 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 5
US-08-470-702-13
; Sequence 13, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 02-MAR-1994  
APPLICATION NUMBER: US/08/470,702  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: US 08/204,656  
FILING DATE: 02-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WEINER, MARC S.  
REGISTRATION NUMBER: 32,181  
REFERENCE/DOCKET NUMBER: 234-252P  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-470-702-13

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-470-702-13 (1-8)

Qy 2 TTGGCACT 10  
Db 3 PheGlyThr 5

RESULT 6  
US-08-467-831-13  
Sequence 13, Application US/08467831  
Patent No. 5635378  
GENERAL INFORMATION:  
APPLICANT: MATSUI, IKUO  
APPLICANT: ISHIKAWA, KAZUHIKO  
APPLICANT: MIYAIRI, SACHIO  
APPLICANT: HONDA, KOICHI  
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE.  
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING  
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
STREET: 8110 Gatehouse Road, Suite 500 East  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22042  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,831

FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/204,656  
FILING DATE: 02-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WEINER, MARC S.  
REGISTRATION NUMBER: 32,181  
REFERENCE/DOCKET NUMBER: 234-252P  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-467-831-13

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-467-831-13 (1-8)

Qy 2 TTGGCACT 10  
Db 3 PheGlyThr 5

RESULT 7  
US-08-331-657-3  
Sequence 3, Application US/08331657  
Patent No. 5783183  
GENERAL INFORMATION:  
APPLICANT: Langeveld, Pieter C.  
APPLICANT: Van Solingen, Pieter  
APPLICANT: Stark, Jacobus  
APPLICANT: Vollebregt, Adrianus W.H.  
TITLE OF INVENTION: Cloning of the zymocin gene and use of  
TITLE OF INVENTION: zymocin in beverages  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,657  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 4615-0049.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Williopsis mrakii  
; STRAIN: IFO 895  
; IMMEDIATE SOURCE:  
; CLONE: Peptide2  
US-08-331-657-3

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-331-657-3 (1-8)

Qy 2 TTGGCACT 10  
Db 2 PheGlyThr 4

RESULT 8  
US-08-571-985-16  
; Sequence 16, Application US/08571985  
; Patent No. 5783557  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Yigal  
; APPLICANT: Trainin, Nathan  
; APPLICANT: Rycus, Avigail  
; TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
; TITLE OF INVENTION: Compositions Comprising Them  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kohn & Associates  
; STREET: 30500 No. 5783557thwestern Hwy., Suite 410  
; CITY: Farmington Hills  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48334  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/571,985  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 106214  
; FILING DATE: 01-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: 2163.00048  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 539-5050  
; TELEFAX: (810) 539-5055  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-571-985-16

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-571-985-16 (1-8)

Qy 9 GTGCCAAG 1  
Db 4 ValProlys 6

RESULT 9  
US-08-408-604A-181  
; Sequence 181, Application US/08408604A  
; Patent No. 5801149  
; GENERAL INFORMATION:  
; APPLICANT: Shoelson, Steven  
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES  
; NUMBER OF SEQUENCES: 211  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,604A  
; FILING DATE: 21-MAR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/134,558  
; FILING DATE: 08-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/959,949  
; FILING DATE: 09-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/722,359  
; FILING DATE: 19-JUNE-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Louis  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: JDP-014CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 181:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-408-604A-181

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0  
US-10-070-588A-112 (1-11) x US-08-408-604A-181 (1-8)  
Qy 10 AGTGCCAAA 2  
Db 5 SerAlaLys 7  
RESULT 10  
US-08-408-604A-207  
; Sequence 207, Application US/08408604A  
; Patent No. 5801149  
; GENERAL INFORMATION:  
; APPLICANT: Shoelson, Steven  
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES  
; NUMBER OF SEQUENCES: 211  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,604A  
; FILING DATE: 21-MAR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/134,558  
; FILING DATE: 08-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/959,949  
; FILING DATE: 09-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/722,359  
; FILING DATE: 19-JUNE-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Louis  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: JDP-014CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 207:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-408-604A-207  
Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
US-10-070-588A-112 (1-11) x US-08-408-604A-207 (1-8)  
Qy 10 AGTGCCAAA 2  
Db 5 SerAlaLys 7  
RESULT 11  
US-08-633-760-3  
; Sequence 3, Application US/08633760  
; Patent No. 5804429  
; GENERAL INFORMATION:  
; APPLICANT: NIWA, MINEO  
; APPLICANT: SAITO, YOSHIMASA  
; APPLICANT: FUJIMURA, TAKAO  
; APPLICANT: ISHII, YOSHINORI  
; APPLICANT: NOGUCHI, YUJI  
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,760  
; FILING DATE: 01-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 18-929-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-633-760-3  
Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
US-10-070-588A-112 (1-11) x US-08-633-760-3 (1-8)  
Qy 3 TTGGCACTA 11  
Db 5 LeuAlaLeu 7  
RESULT 12  
US-08-668-871-9  
; Sequence 9, Application US/08668871  
; Patent No. 5811389  
; GENERAL INFORMATION:  
; APPLICANT: Bannwarth, Wilhelm  
; APPLICANT: Gerber, Fernand  
; APPLICANT: Grieder, Alfred  
; APPLICANT: Knieringer, Andreas  
; APPLICANT: Mueller, Klaus  
; APPLICANT: Obrecht, Daniel  
; APPLICANT: Trzeciak, Arnold  
; TITLE OF INVENTION: TRI- AND TETRACYCLIC COMPOUNDS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/668,871  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,508  
FILING DATE:  
APPLICATION NUMBER: CH 2725/92  
FILING DATE: 31-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kass, Alan P  
REGISTRATION NUMBER: 32142  
REFERENCE/DOCKET NUMBER: RAN 4781/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-4205  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-668-871-9

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-668-871-9 (1-8)

Qy 3 TTGGCACTA 11  
Db 5 LeuAlaLeu 7

RESULT 13  
US-08-669-683-9  
Sequence 9, Application US/08669683  
Patent No. 5811548  
GENERAL INFORMATION:  
APPLICANT: Bannwarth, Wilhelm  
APPLICANT: Gerber, Fernand  
APPLICANT: Grieder, Alfred  
APPLICANT: Knierringer, Andreas  
APPLICANT: Mueller, Klaus  
APPLICANT: Obrecht, Daniel  
APPLICANT: Trzeciak, Arnold  
TITLE OF INVENTION: TRI- AND TETRACYCLIC COMPOUNDS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,683  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,508  
FILING DATE:  
APPLICATION NUMBER: CH 2725/92  
FILING DATE: 31-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kass, Alan P  
REGISTRATION NUMBER: 32142  
REFERENCE/DOCKET NUMBER: RAN 4781/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-4205  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-669-683-9

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-669-683-9 (1-8)

Qy 3 TTGGCACTA 11  
Db 5 LeuAlaLeu 7

RESULT 14  
US-08-482-651-51  
Sequence 51, Application US/08482651  
Patent No. 5874409  
GENERAL INFORMATION:  
APPLICANT: Victoria, Edward J.  
APPLICANT: Marquis, David M.  
TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES  
TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED  
TITLE OF INVENTION: PATHOLOGIES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,651  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Park, Freddie K.  
REGISTRATION NUMBER: 35,636  
REFERENCE/DOCKET NUMBER: 25231-20061.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-482-651-51

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-482-651-51 (1-8)

Qy 3 TTGGCACTA 11  
Db 3 LeuAlaLeu 5

RESULT 15  
US-08-968-676-163  
Sequence 163, Application US/08968676  
Patent No. 5919639  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Sharlene  
APPLICANT: Xu, Minzhen  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,676  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 163:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-968-676-163

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-968-676-163 (1-8)

Qy 10 AGTGCCAAA 2  
Db 4 SerAlaLys 6

RESULT 16  
US-09-016-366A-53  
Sequence 53, Application US/09016366A  
Patent No. 5955431  
GENERAL INFORMATION:  
APPLICANT: Stevens, Richard L.  
APPLICANT: Huang, Chifu  
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE  
TITLE OF INVENTION: INHIBITORS  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02210-2211  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,366A  
FILING DATE: January 30, 1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/037,090  
FILING DATE: 05-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7093  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
TELEX:  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-016-366A-53

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-016-366A-53 (1-8)

Qy 3 TTGGCACTA 11  
Db 2 LeuAlaLeu 4

RESULT 17  
US-09-116-766-16  
Sequence 16, Application US/09116766  
Patent No. 5968898  
GENERAL INFORMATION:  
APPLICANT: Burstein, Yigal

APPLICANT: Trainin, Nathan  
APPLICANT: Rycus, AviGail  
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
TITLE OF INVENTION: Compositions Comprising Them  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 596898thwestern Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/09/116,766  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106214  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Montgomery, Ilene N.  
REGISTRATION NUMBER: 38,972  
REFERENCE/DOCKET NUMBER: 2163.00050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-116-766-16

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-116-766-16 (1-8)

Qy 9 GTGCCAAAG 1  
Db 4 ValProllys 6

RESULT 18  
US-08-310-912A-123  
; Sequence 123, Application US/08310912A  
; Patent No. 5981730  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staekawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 208  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston

STATE: MA  
COUNTRY: USA  
ZIP: 02110-2904  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION NUMBER: US/08/310,912A  
FILING DATE: September 22, 1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/227,360  
FILING DATE: April 13, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lech, Karen F.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/254001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 100254  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-310-912A-123

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-310-912A-123 (1-8)

Qy 3 TTGGCACTA 11  
Db 4 LeuAlaLeu 6

RESULT 19  
US-08-310-912A-125  
; Sequence 125, Application US/08310912A  
; Patent No. 5981730  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staekawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 208  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B



```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-310-912A-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-310-912A-125 (1-8)

Qy 3 TTGGCACTA 11
Db 4 Leulalaleu 6

RESULT 20
US-08-444-818-366
; Sequence 366, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 367:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-367

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-366

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-366 (1-8)

Qy 1 CTTTGGCAC 9
Db 6 LeuTriphis 8

RESULT 21
US-08-444-818-367
; Sequence 367, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 367:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-367

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
```

US-10-070-588A-112 (1-11) x US-08-444-818-367 (1-8)

Qy 1 CTTTGGCAC 9  
Db 5 LeuTrpHis 7

RESULT 22

US-08-444-818-368  
; Sequence 368, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508)359-3876  
; TELEFAX: (508)359-3885  
; INFORMATION FOR SEQ ID NO: 368:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-444-818-368

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-368 (1-8)

Qy 1 CTTTGGCAC 9  
Db 4 LeuTrpHis 6

RESULT 23

US-08-444-818-369  
; Sequence 369, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines

NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Harbin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 369:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-444-818-369

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-369 (1-8)

Qy 1 CTTTGGCAC 9  
Db 3 LeuTrpHis 5

RESULT 24

US-08-444-818-387  
; Sequence 387, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818

; FILING DATE: 424  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Allie A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508)359-3876  
; TELEFAX: (508)359-3885  
; INFORMATION FOR SEQ ID NO: 387:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-444-818-387

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-387 (1-8)

Qy 3 TTGGCACTA 11  
| | | | | | | |  
Db 1 LeuAlaLeu 3

## RESULT 25

US-09-296-284-14  
; Sequence 14, Application US/09296284A  
; Patent No. 6204040  
; GENERAL INFORMATION:  
; APPLICANT: Choi, Eui-Sung  
; APPLICANT: Rhee, Sang-Ki  
; APPLICANT: Lee, Eun-Hae  
; TITLE OF INVENTION: Gluconobacter Suboxydians Sorbitol Dehydrogenase, Genes  
; TITLE OF INVENTION: and Methods of Use Thereof  
; FILE REFERENCE: 1533.0870000  
; CURRENT APPLICATION NUMBER: US/09/296,284A  
; CURRENT FILING DATE: 1999-04-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 8  
; TYPE: PPT  
; ORGANISM: Gluconobacter suboxydians  
US-09-296-284-14

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-296-284-14 (1-8)

Qy 9 GTGCCAAAG 1  
| | | | | | | |  
Db 6 ValProlys 8

## RESULT 26

US-08-660-092-54  
; Sequence 54, Application US/08660092

; Patent No. 6207160  
; GENERAL INFORMATION:  
; APPLICANT: Victoria, Edward J.  
; APPLICANT: Marquis, David M.  
; APPLICANT: Jones, David S.  
; APPLICANT: Yu, Lin  
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES  
; TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED  
; TELECOMMUNICATION INFORMATION: PATHOLOGIES  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,092  
; FILING DATE: 06-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Park, Freddie K.  
; REGISTRATION NUMBER: 35,636  
; REFERENCE/DOCKET NUMBER: 25231-20061.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-660-092-54  
Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-070-588A-112 (1-11) x US-08-660-092-54 (1-8)  
Qy 3 TTGGCACTA 11  
| | | | | | | |  
Db 3 LeuAlaLeu 5  
RESULT 27  
US-08-660-092-188  
; Sequence 188, Application US/08660092  
; Patent No. 6207160  
; GENERAL INFORMATION:  
; APPLICANT: Victoria, Edward J.  
; APPLICANT: Marquis, David M.  
; APPLICANT: Jones, David S.  
; APPLICANT: Yu, Lin  
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES  
; TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED  
; TELECOMMUNICATION INFORMATION: PATHOLOGIES  
; NUMBER OF SEQUENCES: 216  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO

```
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,092
; FILING DATE: 06-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Park, Freddie K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 25231-20061.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /label= Hc
; OTHER INFORMATION: /note= "homocysteine"
;
US-08-660-092-188

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-660-092-188 (1-8)

QY 3 TTGGCACTA 11
| | | | |
Db 5 LeuAlaLeu 7

RESULT 28
US-09-301-085-123
; Sequence 123, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
;
US-09-301-085-123

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-301-085-123 (1-8)

QY 3 TTGGCACTA 11
| | | | |
Db 5 LeuAlaLeu 7

RESULT 28
US-09-301-085-123
; Sequence 123, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
;
US-09-301-085-123
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```
; SEQ ID NO 123
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
;
US-09-301-085-123

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-301-085-123 (1-8)

QY 3 TTGGCACTA 11
| | | | |
Db 4 LeuAlaLeu 6

RESULT 29
US-09-301-085-125
; Sequence 125, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
;
US-09-301-085-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-301-085-125 (1-8)

QY 3 TTGGCACTA 11
| | | | |
Db 4 LeuAlaLeu 6

RESULT 30
US-09-394-630-19
; Sequence 19, Application US/09394630
; Patent No. 6395306
; GENERAL INFORMATION:
; APPLICANT: Cui, Xiangmin
; APPLICANT: Lu, Yuefeng
; APPLICANT: Pan Pacific Pharmaceutical, Inc.
; TITLE OF INVENTION: Useful Properties of a Bee Venom Protein and Gene
```

;; TITLE OF INVENTION: Encoding Same  
;; FILE REFERENCE: 019049-000200US  
;; CURRENT APPLICATION NUMBER: US/09/394,630  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: US 60/100,172  
;; PRIOR FILING DATE: 1998-09-14  
;; NUMBER OF SEQ ID NOS: 22  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 19  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:peptide  
;; OTHER INFORMATION: fragment #88 from in-gel trypsin digestion  
;; NAME/KEY: MOD RES  
;; LOCATION: (1)-(2)  
;; OTHER INFORMATION: Xaa = unsure amino acid  
US-09-394-630-19

Alignment Scores:                    Length:                    8  
Pred. No.:                    1.85e+07                    3  
Score:                    3.00                    Matches:                    3  
Percent Similarity:                    100.00%                    Conservative:                    0  
Best Local Similarity:                    100.00%                    Mismatches:                    0  
Query Match:                    100.00%                    Indels:                    0  
DB:                    3                    Gaps:                    0

US-10-070-588A-112 (1-11) x US-09-394-630-19 (1-8)

Qy                    9 GTGCCAAG 1  
                  |||||  
Db                    6 ValProLys 8

RESULT 31

US-09-160-513-54  
; Sequence 54, Application US/09160513  
; Patent No. 6410775  
; GENERAL INFORMATION:  
; APPLICANT: Victoria, Edward J.  
; APPLICANT: Marquis, David M.  
; APPLICANT: Jones, David S.  
; APPLICANT: Yu, Lin  
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/160,513  
; APPLICATION NUMBER: US/09/160,513  
; FILING DATE: 1998-DEC-24  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CATHERINE M. POLIZZI  
; REGISTRATION NUMBER: 40,130  
; REFERENCE/DOCKET NUMBER: 25231-20061.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid

;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-09-160-513-54  
Alignment Scores:                    Length:                    8  
Pred. No.:                    1.85e+07                    3  
Score:                    3.00                    Matches:                    3  
Percent Similarity:                    100.00%                    Conservative:                    0  
Best Local Similarity:                    100.00%                    Mismatches:                    0  
Query Match:                    100.00%                    Indels:                    0  
DB:                    4                    Gaps:                    0

US-10-070-588A-112 (1-11) x US-09-160-513-54 (1-8)

Qy                    3 TTGCACTA 11  
                  |||||  
Db                    3 LeuAlaLeu 5

RESULT 32

US-09-160-513-188  
; Sequence 188, Application US/09160513  
; Patent No. 6410775  
; GENERAL INFORMATION:  
; APPLICANT: Victoria, Edward J.  
; APPLICANT: Marquis, David M.  
; APPLICANT: Jones, David S.  
; APPLICANT: Yu, Lin  
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/160,513  
; APPLICATION NUMBER: US/09/160,513  
; FILING DATE: 1998-DEC-24  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CATHERINE M. POLIZZI  
; REGISTRATION NUMBER: 40,130  
; REFERENCE/DOCKET NUMBER: 25231-20061.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 188:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /label= Hc  
; OTHER INFORMATION: /note= "homocysteine"  
US-09-160-513-188

Alignment Scores:                    Length:                    8  
Pred. No.:                    1.85e+07                    3  
Score:                    3.00                    Matches:                    3  
Percent Similarity:                    100.00%                    Conservative:                    0  
Best Local Similarity:                    100.00%                    Mismatches:                    0

Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-160-513-188 (1-8)

Qy 3 TTGGCACTA 11  
Db 5 LeuAlaLeu 7

## RESULT 33

US-09-675-922-22  
; Sequence 22, Application US/09675922  
; Patent No. 6468731  
; GENERAL INFORMATION:  
; APPLICANT: Hubbell A., Jeffrey  
; APPLICANT: Schense C., Jason  
; APPLICANT: Sakiyama E., Shelley  
; TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue  
; FILE REFERENCE: ETH 107 DIV  
; CURRENT APPLICATION NUMBER: US/09/675,922  
; CURRENT FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: ACETYLATION Acetylated Glycine  
; OTHER INFORMATION: Description of Artificial Sequence: substrate  
; OTHER INFORMATION: sequence for protease  
US-09-675-922-22

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-675-922-22 (1-8)

Qy 3 TTGGCACTA 11  
Db 3 LeuAlaLeu 5

## RESULT 34

US-09-704-251-15  
; Sequence 15, Application US/09704251  
; Patent No. 6548477  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Gary L.  
; APPLICANT: Self, Christopher  
; APPLICANT: Lee, Lily  
; APPLICANT: Cook, Charles M.  
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE  
; FILE REFERENCE: PPI-106  
; CURRENT APPLICATION NUMBER: US/09/704,251  
; CURRENT FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Motifs  
US-09-704-251-15

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-704-251-15 (1-8)

Qy 3 TTGGCACTA 11  
Db 3 LeuAlaLeu 5

## RESULT 35

US-08-635-886C-124  
; Sequence 124, Application US/08635886C  
; Patent No. 6555114  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROELS, Geert  
; APPLICANT: DELEYS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C  
; FILE REFERENCE: 2752-18  
; CURRENT APPLICATION NUMBER: US/08/635,886C  
; CURRENT FILING DATE: 1996-04-25  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; PRIOR APPLICATION NUMBER: EP 93402718.6  
; PRIOR FILING DATE: 1993-11-04  
; NUMBER OF SEQ ID NOS: 286  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 124  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-08-635-886C-124

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-635-886C-124 (1-8)

Qy 1 CTTTGGCAC 9  
Db 5 Leutrphis 7

## RESULT 36

US-08-635-886C-125  
; Sequence 125, Application US/08635886C  
; Patent No. 6555114  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROELS, Geert  
; APPLICANT: DELEYS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C  
; FILE REFERENCE: 2752-18  
; CURRENT APPLICATION NUMBER: US/08/635,886C  
; CURRENT FILING DATE: 1996-04-25  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; PRIOR APPLICATION NUMBER: EP 93402718.6  
; PRIOR FILING DATE: 1993-11-04  
; NUMBER OF SEQ ID NOS: 286  
; SOFTWARE: Patent in version 3.1  
US-08-635-886C-125

```
; SEQ ID NO 125
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa is Ile, Val, Phe or Leu
US-08-635-886C-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-635-886C-125 (1-8)
Qy 1 CTTTGGCAC 9
Db 1 Leutirphis 3

RESULT 37
US-08-964-747-8
; Sequence 8, Application US/08964747
; Patent No. 659664
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, Tetsuya
; APPLICANT: Granger, Gale A.
; TITLE OF INVENTION: Isolated Tumor Necrosis Factor Receptor
; TITLE OF INVENTION: Releasing Enzyme, Compositions Comprising the Enzyme and
; TITLE OF INVENTION: Methods of the Use Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,747
; FILING DATE: 05-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 3666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858)535-9001
; TELEFAX: (858)535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa is Gln or Ile (Q/I)"
; FEATURE:

; SEQ ID NO 126
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa is Ile, Val, Phe or Leu
US-08-635-886C-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-964-747-8 (1-8)
Qy 3 TTGGCACTA 11
Db 1 LeuAlaLeu 3

RESULT 38
US-09-562-913-8
; Sequence 8, Application US/09562913
; Patent No. 6573062
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, Tetsuya
; APPLICANT: Granger, Gale A.
; TITLE OF INVENTION: Isolated Tumor Necrosis Factor Receptor
; TITLE OF INVENTION: Releasing Enzyme, Compositions Comprising the Enzyme and
; TITLE OF INVENTION: Methods of the Use Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/562,913
; FILING DATE: 02-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 3666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858)535-9001
; TELEFAX: (858)535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa is Gln or Ile (Q/I)"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Xaa is Ser or Pro (S/P)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-562-913-8
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Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-562-913-8 (1-8)

Qy 3 TTGGCACTA 11  
| | | | | | | |  
Db 1 LeuAlaLeu 3

## RESULT 39

US-09-269-439-12  
; Sequence 12, Application US/09269439  
; Patent No. 6610649  
; GENERAL INFORMATION:  
; APPLICANT: Johansson, Bo-Lennart  
; APPLICANT: Jorvall, Hans  
; TITLE OF INVENTION: INSULIN C-PEPTIDES  
; FILE REFERENCE: 08269/008001  
; CURRENT APPLICATION NUMBER: US/09/269,439  
; EARLIER FILING DATE: 1999-07-08  
; EARLIER APPLICATION NUMBER: PCT/GB97/02627  
; EARLIER FILING DATE: 1997-09-26  
; EARLIER APPLICATION NUMBER: SE96/03533-2  
; EARLIER FILING DATE: 1996-09-27  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-269-439-12

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-269-439-12 (1-8)

Qy 3 TTGGCACTA 11  
| | | | | | | |  
Db 1 LeuAlaLeu 3

## RESULT 40

US-08-974-690C-124  
; Sequence 124, Application US/08974690C  
; Patent No. 6613333  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROELS, Geert  
; APPLICANT: DELEYS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C  
; FILE REFERENCE: 2551-94  
; CURRENT APPLICATION NUMBER: US/08/974,690C  
; CURRENT FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; PRIOR APPLICATION NUMBER: EP 93402718.6  
; PRIOR FILING DATE: 1993-11-04  
; NUMBER OF SEQ ID NOS: 286  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 124

; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-08-974-690C-124  
Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-974-690C-124 (1-8)

Qy 1 CTTTGGCAC 9  
| | | | | | | |  
Db 5 LeuTriHis 7

## RESULT 41

US-08-974-690C-125  
; Sequence 125, Application US/08974690C  
; Patent No. 6613333  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROELS, Geert  
; APPLICANT: DELEYS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C  
; FILE REFERENCE: 2551-94  
; CURRENT APPLICATION NUMBER: US/08/974,690C  
; CURRENT FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; PRIOR APPLICATION NUMBER: EP 93402718.6  
; PRIOR FILING DATE: 1993-11-04  
; NUMBER OF SEQ ID NOS: 286  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 125  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (8)-(8)  
; OTHER INFORMATION: Xaa is Ile, Val, Phe or Leu  
US-08-974-690C-125

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-974-690C-125 (1-8)

Qy 1 CTTTGGCAC 9  
| | | | | | | |  
Db 1 LeuTriHis 3

## RESULT 42

US-09-721-108-186  
; Sequence 186, Application US/09721108  
; Patent No. 6664374  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES COMPRISING IL-6 LIGAND-BINDING RECEPTOR  
; TITLE OF INVENTION: DOMAINS AND RELATED NUCLEIC ACIDS, ANTIBODIES,  
; TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 207474  
; CURRENT APPLICATION NUMBER: US/09/721,108



;; CURRENT FILING DATE: 2000-11-22  
;; PRIOR APPLICATION NUMBER: PCT/US00/23490  
;; PRIOR FILING DATE: 2000-08-25  
;; PRIOR APPLICATION NUMBER: US 60/151,277  
;; PRIOR FILING DATE: 1999-08-27  
;; NUMBER OF SEQ ID NOS: 309  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 186  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Binding peptide  
US-09-721-108-186

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-721-108-186 (1-8)

Qy 2 TTGTGCAC 10  
Db 6 PheGlyThr 8

## RESULT 43

US-08-974-685-124  
; Sequence 124, Application US/08974685

; Patent No. 6689368

; GENERAL INFORMATION:

; APPLICANT: LEROUX-ROELS, GEERT  
; DELEYS, ROBERT  
; MAERTENS, GEERT

; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF  
; HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND  
; THERAPEUTIC COMPOSITIONS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 181

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,685  
; FILING DATE: 19-NO. 6689368-1997  
; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 1487-11  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 124:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 124:

US-08-974-685-124

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-974-685-124 (1-8)

Qy 1 CTTTGGCAC 9  
Db 5 LeuTrpHis 7

## RESULT 44

US-08-974-685-125  
; Sequence 125, Application US/08974685

; Patent No. 6689368

; GENERAL INFORMATION:

; APPLICANT: LEROUX-ROELS, GEERT  
; DELEYS, ROBERT  
; MAERTENS, GEERT

; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF  
; HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND  
; THERAPEUTIC COMPOSITIONS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 181

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,685  
; FILING DATE: 19-NO. 6689368-1997  
; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 1487-11  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 125:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: misc-feature

; LOCATION: 8

; OTHER INFORMATION: Xaa is Ile or Val or Phe or Leu

; SEQUENCE DESCRIPTION: SEQ ID NO: 125:

US-08-974-685-125

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-974-685-125 (1-8)

QY 1 CTTTGCAC 9  
| | | | |  
Db 1 LeuTrpHis 3

## RESULT 45

US-09-707-263A-10  
; Sequence 10, Application US/09707263A  
; Patent No. 6696546

; GENERAL INFORMATION:  
; APPLICANT: Bond, Gareth L

; APPLICANT: Manley, James L  
; APPLICANT: Prives, Carol

; TITLE OF INVENTION: A Peptide That Kills Growing But No. 6696546 Stationary Cells  
; FILE REFERENCE: 63331

; CURRENT APPLICATION NUMBER: US/09/707,263A  
; CURRENT FILING DATE: 2000-11-06

; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10  
; LENGTH: 8

; TYPE: PRT  
; ORGANISM: Homo Sapiens

US-09-707-263A-10

## Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-070-588A-112 (1-11) x US-09-707-263A-10 (1-8)

QY 10 AGTGCCAAA 2  
| | | | |  
Db 1 SerAlaLys 3

## RESULT 46

US-09-707-263A-17  
; Sequence 17, Application US/09707263A  
; Patent No. 6696546

; GENERAL INFORMATION:  
; APPLICANT: Bond, Gareth L

; APPLICANT: Manley, James L  
; APPLICANT: Prives, Carol

; TITLE OF INVENTION: A Peptide That Kills Growing But No. 6696546 Stationary Cells  
; FILE REFERENCE: 63331

; CURRENT APPLICATION NUMBER: US/09/707,263A  
; CURRENT FILING DATE: 2000-11-06

; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17  
; LENGTH: 8

; TYPE: PRT  
; ORGANISM: Homo Sapiens

US-09-707-263A-17

## Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-070-588A-112 (1-11) x US-09-707-263A-17 (1-8)

QY 10 AGTGCCAAA 2  
| | | | |  
Db 1 SerAlaLys 3

## RESULT 47

US-09-403-269-4

; Sequence 4, Application US/09403269  
; Patent No. 6764844

; GENERAL INFORMATION:  
; APPLICANT: ULF, Lindahl

; APPLICANT: LI, Jin-Ping  
; TITLE OF INVENTION: DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a

; Patent No. 6764844  
; TITLE OF INVENTION: Process for Its Production

; FILE REFERENCE: 003300-589  
; CURRENT APPLICATION NUMBER: US/09/403,269

; CURRENT FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: SE 9701454-2

; PRIOR FILING DATE: 1997-04-18  
; PRIOR APPLICATION NUMBER: PCT/SE98/00703

; PRIOR FILING DATE: 1998-04-17  
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4

; LENGTH: 8  
; TYPE: PRT

; ORGANISM: Human  
; NAME/KEY: PEPTIDE

; LOCATION: (4)...(4)  
; OTHER INFORMATION: Amino acid 4 is Xaa wherein Xaa = any amino acid.

US-09-403-269-4

## Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-070-588A-112 (1-11) x US-09-403-269-4 (1-8)

QY 9 GTGCCAAG 1  
| | | | |  
Db 6 ValProLys 8

## RESULT 48

US-09-261-894A-163

; Sequence 163, Application US/09261894A  
; Patent No. 6835382

; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT E.

; APPLICANT: ADAMS, SHARLENE  
; APPLICANT: XU, MINZHEN

; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION  
; FILE REFERENCE: REH-2006

; CURRENT APPLICATION NUMBER: US/09/261,894A  
; CURRENT FILING DATE: 1999-03-03

; NUMBER OF SEQ ID NOS: 167  
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 163  
; LENGTH: 8

; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide  
US-09-261-894A-163

## Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-070-588A-112 (1-11) x US-09-261-894A-163 (1-8)

Oy 10 AGTGCCAA 2  
| | | | |  
Db 4 SerAlaLeu 6

## RESULT 49

PCT-US95-04589-123  
; Sequence 123, Application PC/TUS9504589  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF  
; NUMBER OF SEQUENCES: 201  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street Suite 3100  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04589  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,360  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/230001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 100254  
; INFORMATION FOR SEQ ID NO: 123:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-04589-123

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-070-588A-112 (1-11) x PCT-US95-04589-123 (1-8)

Oy 3 TTGGCACTA 11  
| | | | |  
Db 4 LeuAlaLeu 6

## RESULT 50

PCT-US95-04589-125  
; Sequence 125, Application PC/TUS9504589

; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF  
; NUMBER OF SEQUENCES: 201  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street Suite 3100  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04589  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,360  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/230001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 100254  
; INFORMATION FOR SEQ ID NO: 125:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-04589-125

Alignment Scores:  
Pred. No.: 1.85e+07 Length: 8  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-070-588A-112 (1-11) x PCT-US95-04589-125 (1-8)

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Search completed: March 12, 2005, 11:08:45  
Job time : 22 secs

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